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GenCore version 5.1.6
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OM protein - protein search, using sw model

7, 2004, 18:17:14 ; Search time 50.5 Seconds (without alignments) 1818.375 Million cell updates/sec July Run on:

US-10-720-192-2

Title:

1726 1 MHQVDPNLTRRKGRLAALAI.......PAGEVAPTPTTPTPQRTLPA 325 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

1586107 segs, 282547505 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08 Maximum Match 1008 Listing first 45 summaries

geneseqp2001s:\*
geneseqp2002s:\*
geneseqp2003as:\*
geneseqp2003bs:\* A Geneseq 29Jan04:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| SUMMARIES | Description   | 565 Aycobacte | 2 Aam50732 | 50 Aaw32350 | 18 Aaw32418 | 22 Aaw64322   | 3 Aaw81683 | 5 Aay38945 M. | 3 Aay3908 | 5 Aau 0189 | 720 Aae29720 Mycobacte | 4 Aae17584    | 1 Aay9728 | 9       | Aay39082 | 225 Aay39225 M. tuberc | Aaw6437  | Aaw81746 | 3 Aay3206 | 3 Aay39033 | Aay3908  | 6 Aay39176 M. | Aay3922  | 92     | 7       | 42 Abu52942 |
|-----------|---------------|---------------|------------|-------------|-------------|---------------|------------|---------------|-----------|------------|------------------------|---------------|-----------|---------|----------|------------------------|----------|----------|-----------|------------|----------|---------------|----------|--------|---------|-------------|
| SC        | Ü             | AAW0356       | AAM5073    | AAW323      | AAW3241     | <b>AAW643</b> | AAW8168    | AAY3894       | AAY3908   | AAU018     | AAE2972                | <b>AAE175</b> | AAY9728   | AAW0356 | AAY39082 | AAY3922                | AAW64379 | AAW81746 | AAY3206   | AAY3903    | AAY39081 | AAY3917       | AAY39224 | AAU745 | ADB7434 | ARII529     |
|           | DB            | 5             | Ŋ          | 7           | 7           | C)            | (1         | N             | N         | 4          | Ŋ                      | ß             | n         | N       | N        | N                      | N        | N        | N         | N          | (1)      | N             | N        | 'n     | ۲       | 4           |
|           | Leng          | 325           | 325        | 332         | 332         | 332           | 332        | 332           | 332       | 332        | 332                    | 332           | 325       | 286     | 652      | 652                    | 802      | 802      | 802       | 802        | 802      | 802           | 802      | 802    | 287     | 268         |
| *         | ery           | 100.0         | 100.0      | 100.0       | 100.0       | 100.0         | 100.0      | 100.0         | 100.0     | 100.0      | 100.0                  | 100.0         | 99.7      | 89.3    | 86.8     | 86.8                   | 86.8     | 86.8     | 86.8      | 86.8       | 86.8     | 86.8          | 86.8     | 86.8   | 56.8    | α,          |
|           | Score         | 1726          | 72         | 1726        | 72          | 72            | 72         | 72            | 72        | 72         | 72                     | 72            | 72        | 54      | 49       | 49                     | 9        | 9        | 49        | 49         | 49       | g             | 4        | 49     | œ       |             |
|           | Result<br>No. |               | 7          | ٣           | 4           | വ             | 9          | 7             | ω         | σ          | 10                     | 11            | 12        | 13      | 14       | 15                     | 16       | 17       | 18        | 19         | 20       | 21            | 22       | 23     | 24      | 25          |

| Abu52945 Human mam | Abu52944 Human mam | Abu52939 Human mam | Abu08487 S. pneumo | Aaq15453 Arabidops | Adbessio Human pro | Abu37030 Protein e | Abb70063 Drosophil | Abb92424 Herbicida | Abu52938 Human mam | Aaw31852 Mycobacte | Abu52932 Human mam |          | Abu52937 Human mam | Abr53281 Protein s | Abu52940 Human mam | Abu52936 Human mam | Abu52933 Human mam | Abg27250 Novel hum | Abu52941 Human mam |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| ABU52945           | ABU52944           | ABU52939           | ABU08487           | AAG15453           | ADB65210           | ABU37030           | ABB70063           | ABB92424           | ABU52938           | AAW31,852          | ABU52932           | ABU52931 | ABU52937           | ABR53281           | ABU52940           | ABU52936           | ABU52933           | ABG27250           | ABU52941           |
| 4                  | 4                  | 4                  | 9                  | m                  | 7                  | 9                  | 4                  | Ŋ                  | 4                  | 7                  | 4                  | 4        | 4                  | 9                  | 4                  | 4                  | 4                  | 4                  | 4                  |
| 256                | 262                | 270                | 8991               | 544                | 652                | 598                | 446                | 652                | 267                | 763                | 260                | 267      | 253                | 817                | 261                | 277                | 254                | 406                | 258                |
| 9.                 | 'n.                | 'n.                | 'n.                | ۲,                 | ς.                 | 7                  | ۲.                 | ٥.                 | σ.                 | o,                 | 2.8                | 2.8      | 2.7                | φ.                 | 5.6                | 9.                 | 'n                 | 4.                 | e.                 |
| 13                 | 13.                | 13                 | 13                 | 13.2               | 13                 | 13                 | 13.                | 12                 | 12.                | 12                 | 12                 | 12       | 17                 | 12                 | 12                 | 12                 | 12                 | 12                 | 12                 |
| 235                | 233.5              | 233                | 233                | 228                | 227.5              | 227                | 225.5              | 223.5              | 222.5              | 222                | 221.5              | 221.5    | 218.5              | 217.5              | 217                | 217                | 216.5              | 214                | 212.5              |
| 26                 | 27                 | 28                 | 29                 | 30                 | 31                 | 32                 | 33                 | 34                 | 35                 | 36                 | 3.3                | 38       | 39                 | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |
|                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |          |                    |                    |                    |                    |                    |                    |                    |

### ALIGNMENTS

RESULT 1 AAW03565

AAW03565 standard; protein; 325 AA

AAW03565;

(first entry) 22-APR-1997 Mycobacterium tuberculosis antigenic determinant protein.

Antigenic determinant; Mycobacterium tuberculosis; ion exchange; human; chromatography; gel filtration; reverse phase column chromatography; immunogenic; serum; quinea pig; expression vector; osemid; antibody; Mycobacterium smegmatis; Mycobacterium bovis BCG; microorganism; vaccine; hybrid; epitope; disease; diphtheria; cholera; toxin. 

Mycobacterium tuberculosis,

1. .39 /note= "signal peptide" 40. .325 /note= "mature protein" Location/Qualifiers Key Peptide Protein

96WO-FR000166. 31-JAN-1996; 08-AUG-1996.

WO9623885-A1

95US-00382184. 01-FEB-1995;

(INSP ) INST PASTEUR.

Romain F; Pescher P, <u>ن</u> Laqueyrerie A, Marchal

WPI; 1996-371433/37. N-PSDB; AAT39357.

Mycobacterium tuberculosis antigen and hybrid proteins comprising it useful in vaccines against tuberculosis and in immunoassays.

Claim 2; Page 49-50; 74pp; French.

This is the amino acid sequence of an antigenic determinant protein from Mycobacterium tuberculosis. The mature protein has calculated mol. wt. of 28779 Da but has an experimental mol. wt of 45-47 kD as determined by SDS -PAGE. The difference is thought to be due to the high frequency of Pro

10-JUL-2001; 2001WO-US021717.

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tuberculosis strain H37Rv by conventional chromatographic methods e.g.
tuberculosis strain H37Rv by conventional chromatographic methods e.g.
low pressure ion exchange chromatography, Si 300 gel filtration, DEAE ion
exchange and reverse phase coluum chromatography. The proteins were then
separated by SDS-PAGE and immunogenic proteins determined with immune
complex of mol wt. 45-47 kb was identified. An expression library of
genomic M. tuberculosis DNA was generated in the cosmid vector pVUB18.
The library was transformed into M.smegmatis. Clones expressing antigenic
determinants were isolated by screening with an antibody against the M.
contained identical sequences 1.e. the sequence presented here. The
protein or microcoganisms expressing it can be used as vaccines against
tuberculosis. Also hybrid proteins comprising this protein and epitopes
from other disease causing organisms or proteins, e.g. diphtheria or
cholera toxin, can be used as vaccines against their respective diseases
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sequence. The protein was purified from M.
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/label= Signal_peptide
/note= "&BC-dependent signal secretion sequence"
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40. .325
/label= Mature_protein
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Best Local Similarity 100.0%;
Matches 325; Conservative 0
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WO200204018-A2

17-JAN-2002

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The present sequence is that of the Mycobacterium tuberculosis (Mtb) strain H37Rv gene Rv1860 product, designated ModD MF732. This is one of AAMS0729-59) discovered or cytosolic Mtb proteins of strain H37Rv (see AAMS0729-59) discovered through the use of 2-dimensional liquid phase electrophoresis coupled with an in vitro interferon-gamma assay and strong chromatography-mass spectrometry. The immunogens stimulate a strong interferon-gamma response from T cells of M. tuberculosis infected mice. The invention provides vaccine compositions for boosting immunity comprobacteria when administered in mid-life to a subject who has been vaccinated neonatally or in early childhood with BcG and in whom protective immunity has waned. The vaccine compositions compities 1 or more of the 31 purified immunogenic proteins. When used as immunogens, the secreted Mtb proteins lack the secreted signal sequence. A preferred protein is Ag85A (see AAMS0759), the secreted product of the Rv3084v gene
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                                                                                                                                                                               Vaccine for boosting immunity to mycobacteria when administered in mid-
life in a subject who has been vaccinated in childhood with Bacillus
Calmette-Guerrin, has purified proteins from mycobacterium tuberculosis.
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100.0%; Pred. No. 1.3e-104;
iive 0; Mismatches 0;
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                                 10-JUL-2000; 2000US-0217646P.
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AAW32418 standard; protein; 332
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                                                                                                                                                                                                                                                                                                                                                                    A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, DPEP. The immunogenic polypeptide can be used to diagnose M.tuberculosis infection by forming complexes with specific antibodies in the sample. Fragments of DNA encoding the immunogenic polypeptide can be used as diagnostic primers or probes and agents that bind to the antigen, especially monoclonal antibodies or equivalent polyclonal antibodies, are also used for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SFALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPPVANDTRIVLGRLDQKLYASAEA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MHQVDPNLTRRKGRLAALAIAAMASASLVTVAVPATANADPEPAPPVPTTAASPPSTAAA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SFALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPPVANDTRIVLGRLDQKLYASAEA
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                                                                                                                                                                                                                                                                                                             tuberculosis antigens
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                                                                                                                                                                                                                                  Houghton R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1726; DB 2;
Pred. No. 1.3e-104;
                                                                                                                                                                                                                                                                                                          New immunogenic polypeptide(s) from soluble M. tukuseful for diagnosis of M. tuberculosis infection.
                                                                                                                                                                                                                                  Campos-Neto A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                Example 1; Page 92-94; 190pp; English
                                                                                                                                                                                                                               eiky YAW, Dillon DC,
Twardzik DR;
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                                                                                                                           95US-00523435.
95US-00532136.
96US-00620280.
96US-00658800.
96US-00688800.
skin testing; M.tuberculosis
                                                                                                   96WO-US014675
                         Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                  Skeiky YAW,
                                                                                                                                                                                                        (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                      WPI; 1997-192904/17
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Best Local Similarity
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                                                                                                                             01-SEP-1995;
22-SEP-1995;
22-MAR-1996;
05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 332
                                                   WO9709429-A2
                                                                                                    30-AUG-1996;
                                                                                                                                                                               12-JUL-1996
                                                                                                                                                                                                                                               Vedvick TH,
                                                                            13-MAR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, DPEP. The immunogenic protein, and fusion proteins containing one or more of the proteins or one of the proteins plus ESAF-6, are useful in vaccines, preferably when formulated with a non-specific adjuvant, to induce an immune response against M.tuberculosis (for treatment or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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also
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                                                                                           Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant; skin testing; M.tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tuberculosis tuberculosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 100.0%; Score 1726; DB 2; Local Similarity 100.0%; Pred. No. 1.3e-104; les 325; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Campos-Neto A,
                                                 Mycobacterium tuberculosis antigen DPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 87-89; 168pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dillon DC,
DR;
                                                                                                                                                                                                                                                                                                                                                                                     95US-00523436.
95US-00533634.
96US-00620874.
96US-00659683.
                                                                                                                                                                                                                                                                                                                                            96WO-US014674
                                                                                                                                                                                   tuberculosis
  entry)
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I, Twardzik
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(first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 332 AA;
                                                                                                                                                                                   Mycobacterium
                                                                                                                                                                                                                                  WO9709428-A2
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248 GVIGSPAANAPDAGPPQRWFVVWLGTANNPVDKGAAKALAESIRPLVAPPPAPAPAEP 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method inducing protective immunity against tuberculosis (TB). This sequence be formulated into vaccines and/or pharmaceutical compositions for diagnosis of tuberculosis infection or may be used for the diagnosis of tuberculosis
                                                                                                                                                               241 GVIGSPAANAPDAGFPQRWFVVWLGTANNPVDKGAAKALAESIRPLVAPPPAPAPAFFP
                                128 SFALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPPVANDTRIVLGRLDQKLYASAEA
                                                                                                                    188 TDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFSDPSKPNGQIWT
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SFALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPPVANDTRIVLGRLDQKLYASAEA
                                                                             TDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFSDPSKPNGQIWT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tuberculosis; immunogenic; soluble; antigen; protective immunity; TB; vaccine; pharmaceutical; infection; diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA -develop products for the detection of M. tuberculosis infection diagnosis, treatment and prevention of tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 1726; DB 2; 100.0%; Pred. No. 1.3e-104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M. tuberculosis immunogenic polypeptide DPEP.
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                                                                                                                                                                                                                                             325
                                                                                                                                                                                                                                                                       308 APAPAAGEVAPTPTTPPQRTLPA 332
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Vedvick TS, Twardzik DR, Lodes MJ;
                                                                                                                                                                                                                                                 APAPAPAGEVAPTPTTPTPQRTLPA
                                                                                                                                                                                                                                                                                                                                                                                         protein; 332 AA
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97US-00818112.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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N-PSDB; AAV64498.
                                                                                                                                                                                                                                                                                                                                                                                            AAW81683 standard;
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325; Conserv
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Best Local S:
Matches 325,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA sequence (see AAV4439) conding for DPEP was isolated from a M. tuberculosis genomic library using a probe based on an isolated Noterminal peptide (see AAV4439). The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAW44291-W64379) comprising an antigenic portion of a soluble M. tuberculosis antigen, as well as DNA sequences encoding such polypeptides, recombinant expression vectors and transformed or transfected host calls. Also claimed are methods and diagnostic kits for detecting M. tuberculosis in a patient using these polypeptides, antibodies or oligonuclectide probes and primers, for the diagnosis of tuberculosis oligonuclectide probes and primers, for the diagnosis of tuberculosis. (Updated on 17-OCT-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This polypeptide comprises the Mycobacterium tuberculosis antigen DPEP. A
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    GVIGSPAANAPDAGPPQRWFVVWLGTANNPVDKGAAKALAESIRPLVAPPPAPAPAPAFP 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated Mycobacterium tuberculosis polypeptides and DNA - used develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Campos-Neto A,
                                                                                                                                                                                                                                                                                                                                                                        Tuberculosis; infection; diagnosis; antigen; DPEP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 1726; DB 2; Best Local Similarity 100.0%; Pred. No. 1.3e-104; Matches 325; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis; strain H37Rv
                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis antigen DPEP
                                                                                  APAPAPAGEVAPTPTTPTPORTLPA 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 93-94; 250pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dillon DC, Ca
DR, Lodes MJ;
                                                                                                                                                                                       AAW64322 standard; protein; 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96US-00729622
97US-00818111
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                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Skeiky YAW,
3, Twardzik
                                                                                                                                                                                                                                                                     (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-251292/22.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-OCT-1996;
13-MAR-1997;
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09-NOV-1998
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                                                                                                                                                                                                                                AAW64322;
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                                                                                                                                                                                                                 188 TDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFSDPSKPNGQIWT 247
                                                                                                                                                                                                                                                                                                                                 248 GVIGSPAANAPDAGPPQRWFVVWLGTANNPVDKGAAKALAESIRPLVAPPPAPAPAPPPA 307
                                                          SPALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPPVANDTRIVLGRLDQKLYASAEA 180
                                                                                                               SFALPAGWVESDAAHFDYGSALLSKTIGDPPFPGQPPVANDTRIVLGRLDQKLYASAEA 187
                                                                                                                                                                                                                                                                                            GVIGSPAANAPDAGPPQRWFVVWLGTANNPVDKGAAKALAESIRPLVAPPPAAPAPARP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes novel recombinant antigens and their encoding
PPAPATPVAPPPPAAANTPNAQPGDPNAAPPPADPNAPPPPVIAPNAPQPVRIDNPVGGF
                                                                                                                                                                            TDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFSDPSKPNGQIWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antigen; diagnosis; detection; infection; antibody; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polypeptide comprising antigenic portions of M. tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Campos-Neto A, Houghton R; J, Hendrickson RC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 1726; DB 2;
100.0%; Pred. No. 1.3e-104;
ive 0; Mismatches 0;

    M. tuberculosis recombinant antigen protein DPBP.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                308 APAPAGEVAPIPITPIPA 332
                                                                                                                                                                                                                                                                                                                                                                                                              301 APAPAPAGEVAPTPTTPQRTLPA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        eiky YAW, Dillon DC, Car
Twardzik DR, Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY38945 standard; protein; 332 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US003265.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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Best Local Similarity 100.
Matches 325; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Skeiky YAW,
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N-PSDB; AAZ19088.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vaccine; immunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 332 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-FEB-1998;
05-MAY-1998;
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Vedvick TS,
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8 MHOVDPNIJTRRKGRLAALAIAAMASASLVIVAVPAIANADPEPAPPVPTIAASPPSIAAA 67

1 MHQVDPNLTRRKGRLAALALAAMASASLVTVAVPATANADPEPAPPVPTTAASPPSTAAA

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                                                                                                                           240
                                                                                                                                                                                                    300
            127
                                                                                                                                                                                                                                      248 GVIGSPAANAPDAGPPORWFVVWLGTANNPVDKGAAKALAESIRPLVAPPPAPPAPAEP 307
                                                                                                                                                           188 TDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFSDPSKPNGQIWT 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions.
PPAPATPVAPPPPAAANTPNAQPGDPNAAPPPADPNAPPPPVIAPNAPQPVRIDNPVGGF
                                                121 SFALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPPVANDTRIVLGRLDQKLYASAEA
                                                                                                                           181 TDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFSDPSKPNGQIWT
                                                                                                                                                                                                      GVIGSPAANAPDAGPPQRWFVVWLGTANNPVDKGAAKALAESIRPLVAPPPAPAPAEP
                                                                                  128 SFALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPPVANDTRIVLGRLDQKLYASAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dillon DC, Campos-Neto A, Houghton R; DR, Lodes MJ, Hendrickson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s; M. tuberculosis; antigen; immunismunisation; vaccine; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M. tuberculosis antigen DPEP amino acid sequence
                                                                                                                                                                                                                                                                               301 APAPAPAGEVAPTPTTPTPQRTLPA 325
                                                                                                                                                                                                                                                                                                                   308 APAPAPAGEVAPTPTTPTPQRTLPA 332
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                                                                                                                                                                                                                                                                                                                                                                                                                AAY39083 standard; protein; 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immune response; skin test.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Skeiky YAW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORI-) CORIXA CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 332 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-MAY-1998;
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patients with acquired immunodeficiency disease, AIDS

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                                                                                                                                       SFALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPPVANDTRIVLGRLDQKLYASAEA
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                                                                                                                                                                                                              1 MHQVDPNLTRRKGRLAALAIAAMASASLVTVAVPATANADPEPAPPVPTTAASPPSTAAA
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                                                                                                    PPAPATPVAPPPPAAANTPNAQPGDPNAAPPPPADPNAPPPVIAPNAPQPVRIDNPVGGF
                                                                                                                         SPALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPPVANDTRIVLGRLDQKLYASAEA
                                                                                                                                                                TDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFSDPSKPNGQIWT
                                                                                                                                                                                  TDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFSDPSKPNGQIWT
                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaccinating against Mycobacteria infections in mammals using fusion proteins comprising combinations of heterologous antigens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lodes
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0
        Length 332;
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                           Indels
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     Score 1726; DB 2;
Pred. No. 1.3e-104;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                           antigen; vaccine; tuberculosis; AIDS;
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100.0%; Sc.
100.0%; Pre
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                                                                                                                                                                                                                                                                                                               protein; 332
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99US-0158425P.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis.
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                           Matches 325; Conservative
                                                                                                                                                                                                                                                                                                                                                                        M. tuberculosis DPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-290576/30.
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                                                                                                                                                                                                                                                                                                               standard;
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                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAS03786
                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200124820-A1
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        Query Match
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The sequence represents Mycobacterium tuberculosis DPEP, an M. tuberculosis antigen. Compositions comprising at least 2 heterologous antigens, as a fusion protein, and vectors expressing the fusion proteins are used as vaccines to prophylactically immunise mammals (especially humans) against infection by Mycobacceria. The compositions contain at least 2 heterologous antigens that increase the serological sensitivity of individuals infected with tuberculosis, a disease frequently affecting

Disclosure; Page 160; 168pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                       248 GVIGSPAANAPDAGPPORWFVVWLGTANNPVDKGAAKALAESIRPLVAPPPAPAPAEP 307
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                                                                                         Gaps
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                                                             Length 332;
                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis DPEP antigenic protein.
                                                          100.0%; Score 1726; DB 4;
100.0%; Pred. No. 1.3e-104;
ive 0; Mismatches 0;
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                                                                              Best Local Similarity 100.
Matches 325; Conservative
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N-PSDB; AAD47097.
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tuberculosis.
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polypeptide or its fragment. The Leishmania polynucleotide is selected from TSA, LeIF, MIS, and 6H polynucleotides. Sequences of the invention are used in methods for eliciting immune response in mammals. They are useful as vaccines to elicit protective immunity against pathogenic microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polynucleotides, as in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is M. tuberculosis DPEP antigenic protein
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                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 1726; DB 5; 100.0%; Pred. No. 1.3e-104;
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01-FEB-2001; 2001US-0265737P.
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tuberculosis; infection;
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N-PSDB; AAD28355.
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The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, mucleotides encoding them and compositions comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase the serological sensitivity of sera from individuals infected with cuberculosis and methods for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention are useful for eliciting an immune response in a mammal, e.g., human, immunised with RCG. They are useful in the diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the Mycobacterium, in vitro and in vivo assays for detecting humoral antibodies or cell-mediated immunity against M. tuberculosis, for the diagnosis to generate or elicit a protective immune response in a munuogens to generate or elicit a protective immune response in a munuogens to generate or elicit a protective immune response in a minimal antibodies in a non-human and an incoming a second antibodies in a non-human and an incoming an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      animal. Sequences of the invention are also used as vaccines. MTB32A fusion proteins of the invention are useful as in vivo diagnostic agents for intradermal skin test. The present sequence is Mycobacterium species
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subject
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  Mycobacterium species, useful for eliciting immune response
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Pred. No. 1.3e-104;
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                                                         Claim 9; Page 127; 136pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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les 325; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DPEP protein
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Matches
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This is the amino acid sequence of the mature potion of an antigenic determinant protein from Mycobacterium tuberculosis. The mature protein has calculated mol. wt. of 2477 bg but has an experimental mol. wt of 45 and 247 kD as determined by SDS-PAGE. The difference is thought to be due to the high frequency of Pro residues (21.7%) in the sequence. The protein was purified from N. tuberculosis strain H37K by conventional chromatographic methods e.g. low pressure ion exchange chromatography. The proteins were then separated by SDS-PAGE and immunogenic proteins determined with immune serum from humans with TB or guinea pigs infected with M. tuberculosis. A complex of mol. wt. 45-47 kD was identified. An expression library of genomic M. tuberculosis DNA was generated in the cosmid vector pyvUBH8. The library was transformed into M. smegmatis. Clones expressing antigenic determinants were isolated by cromes were isolated, all of which contained identical sequences i.e. the sequence presented here. The protein or microorganisms expressing it can be used as vaccines against tuberculosis. Also hybrid proteins comprising this protein and epitopes from other disease causing organisms or
                                                               Antigenic determinant; Mycobacterium tuberculosis; ion exchange; human; chromatography; gel filtration; reverse phase column chromatography; immunogenic; serum; guinea pig; expression vector; cosmid; antibody; Mycobacterium smegmatis; Mycobacterium bovis BGG; microorganism; vaccine; hybrid; epitope; disease; diphtheria; cholera; toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 ANDTRIVLGRLDQXLYASAEATDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40 DPEPAPPVPTTAASPPSTAAAPPAPATPVAPPPPAAANTPNAQPGDPNAAPPPADPNAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DEEPAPPVPITAASPPSTAAAPPAPATPVAPPPPAAANTPNAQPGDPNAAPPPADPNAPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 PPVIAPNAPQPVRIDNPVGGFSFALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANDTRIVLGRLDQKLYASAEATDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis antigen and hybrid proteins comprising it
                        Mycobacterium tuberculosis antigenic determinant mature protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful in vaccines against tuberculosis and in immunoassays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pescher P, Romain F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89.3%; Score 1542; DB 2;
100.0%; Pred. No. 1.1e-92;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteins, e.g. diphtheria or cholo
against their respective diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 49; 74pp; French
                                                                                                                                                                                                                                                                                                                                                                                           95US-00382184.
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                                                                                                                                                                                                         Mycobacterium tuberculosis.
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Best Local Similarity 100.
Matches 286; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                    INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1996-371433/37.
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                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1995;
                                                                                                                                                                                                                                                                                                                                             31-JAN-1996;
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                                                                                                                                                                                                                                                                                                 08-AUG-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A new method of treating an inflammatory response comprises administering a microbial polypeptide which is preferably a mycobacterial polypeptide. The method is particularly useful for treating or inhibiting a Th2 mediated inflammatory response. The inflammatory response is associated with a disease such as skin alergy, hives, allergic rhinitis, or asthma. Specifically, the asthma is intrinsic, i.e. associated with an irritant (e.g. a pathogen causing a respiratory tract infection in a mammal, or an inhaled pollutant). The asthma may also be extrinsic, which includes aspergillosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFSDPSKPNGQIWT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SFALPAGWVESDAAHLDYGSALLSKTTGDPPFPGQPPPVANDTRIVLGRLDQKLYASAEA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                           ng an inflammatory response in a mammal for treating skin allergic rhinitis, hay fever, or asthma comprises administering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MHQVDPNLTRRKGRLAALA1AAMASASLVTVAVPATANADPEPAPPVPTTAASPPSTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MHOVDPNLTRRKGRLAALAIAAMASASLVTVAVPATANADPEPAPPVPTTAASPPSTAAA
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Pred. No. 3.2e-104;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Fig 1; 52pp; English.
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Matches 324; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   allergy, allergic rhinit
a microbial polypeptide
                                                                                                                                                                                                                                                                           Ratliff TL, Kline JN;
                                                                                                                                                                                                                                                                                                                         WPI; 2000-549237/50.
N-PSDB; AAA53822.
Mycobacterium bovis.
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                                           WO200048622-A2
                                                                                                                                                                                    22-FEB-1999;
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287 VAPPPAPAPAPAPAPAPAPAGEVAPTPTTPTPQRTLPA
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                                                                                                                                                                                                                                                                                                                                  05-MAY-1998;
                                                                                                                                                                                                                                                                         26-AUG-1999.
                                                                                                                                                                                                                                                                                                                       18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                          Vedvick TS,
                                                                                                                         05-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          374 VPITAASPPSTAAAPPAAPTFVAPPPAAANTFNAQPGDPNAAPPPADPNAPPPPVIAPN 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           434 APQPVRIDNPVGGFSFALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPPVANDTRIV 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGRLDQKLYASAEATDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEV 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGRLDOKLYASAEATDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEV 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KFSDPSKPNGQIWTGVIGSPAANAPDAGPPQRWFVVWLGTANNPVDKGAAKALAESIRPL 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KESDPSKPNGQIWTGVIGSPAANAPDAGPPQRWFVVWLGTANNPVDKGAAKALAESIRPL 613
 SASYYEVKFSDPSKPNGQIWTGVIGSPAANAPDAGPPQRWFVVWLGTANNPVDKGAAKAL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes novel recombinant antigens and their encoding nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                             Antigen; diagnosis; detection; infection; antibody; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polypeptide comprising antigenic portions of M. tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                               Houghton R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86.8%; Score 1499; DB 2; Length 652; 100.0%; Pred. No. 1.5e-89; cive 0; Mismatches 0; Indels (
                                    AESIRPLVAPPPAPAPAPAPAPAPAGEVAPTPTTPTPQRTLPA 286
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I, Hendrickson RC;
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                                                                                                                                                                                                                                                                                                                                                                             Dillon DC, Cam
DR, Lodes MJ,
                                                                                                                                                                       M tuberculosis fusion protein TbF-8.
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                                                                                                    AAY39082 standard; protein; 652
                                                                                                                                                                                                                                                                                                                       98US-00024753.
                                                                                                                                                                                                                                                                                                  99WO-US003265
                                                                                                                                                                                                                                Mycobacterium tuberculosis.
                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                               Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                          (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-527416/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 279; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAZ19248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 652 AA;
                                                                                                                                                                                                                                                                                                                                                                               Reed SG, Ske
Vedvick TS,
                                                                                                                                                                                                                                                     WO9942118-A2
                                                                                                                                                                                                                                                                                                  17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                    05-MAY-1998;
                                                                                                                                                 05-NOV-1999
                                                                                                                                                                                                                                                                                                                        18-FEB-1998;
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  181
                                              241
                                                                                                                          AAY39082;
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The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's. M. tuberculosis Ag's. DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin teste for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion by, T, B or natural killer cells and/or macrophages in tuberculosis-immune subjects. AAZ19249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    434 APQPVRIDNPVGGFSFALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPPVANDTRIV 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47 VPTTAASPPSTAAAPPAPATPVAPPPPAAANTPNAQPGDPNAAPPPADPNAPPPPVIAPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen; immunotherapy; diagnosis; immunisation; vaccine; infection; immune response; skin test.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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I, Hendrickson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 652;
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                                                                                                                                                                                                                                                                                                                                                                                             M. tuberculosis fusion protein TbF-8 amino acid sequence
325
                                   614 VAPPPAPAPAPABAPAPAPAGEVAPIPITPIPARA 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 37; Page 274-276; 299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dillon DC, Car
DR, Lodes MJ,
                                                                                                                                                                                                                A
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                                                                                                                                                                                                             AAY39225 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                (first entry)
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Best Local Similarity 100.
Matches 279; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-527409/44.
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433 166

Search completed: July 7, 2004, 18:21:03 Job time: 53.5 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

July 7, 2004, 18:19:15; Search time 22.5 Seconds (without alignments) 1389.433 Million cell updates/sec

US-10-720-192-2 1726 1 MHQVDPNLTRRKGRLAALAI......PAGBVAPTPTTPTPQRTLPA 325 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:\*
1: Dirl:\*
2: Dir2:\*
3: Dir3:\*
4: Dir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Description         | probable modD prot | prot       | extensin-like prot | extensin - Volvox | ical |        | 낊      |          | cal    | hypothetical prote | cal    | extensin homolog T | •      | extensin-like cell |            | hypothetical prote |               | Ψ      | 367K tegument prot | ne |        |        | probable Pto kinas |     | homolog | ซ  | ical  | hypothetical prote |
|---------------------|--------------------|------------|--------------------|-------------------|------|--------|--------|----------|--------|--------------------|--------|--------------------|--------|--------------------|------------|--------------------|---------------|--------|--------------------|----|--------|--------|--------------------|-----|---------|----|-------|--------------------|
|                     | D70666             | 161        | 99                 | 269               | 57   | $\sim$ | T44744 | S51342 · | F75518 | T29018             | F96531 | T06291             | WMBEH6 | T10737             | Ϋ́         | T38236             | T28770        | G86441 | WZBEB6             | m  | H75457 | T09854 | F86387             | 9   | T04859  | 72 | 1514  | 80                 |
| h DB                | 101                |            |                    |                   |      |        |        |          |        |                    |        |                    |        |                    |            |                    |               |        |                    |    |        |        |                    |     |         |    |       |                    |
| Length              | 325                | 4 rc       | 118                | 46                | 22   | 353    | 00     | 81       | 83     | 80                 | 84     | 94                 | 316    | 21                 | 41         | 161                | 53            | N      | 342                | 28 | 39     | 21     | 16                 | 70  | 83      | 86 | 41    | 99                 |
| %<br>Query<br>Match | 100.0              | 04         | ຸຕ                 | m                 | m    | ന      | 12.7   | N        | 12.6   | N                  | N      | N                  | N      | 12.1               | $^{\circ}$ | 12.0               | $\overline{}$ | -      | М                  | Н  | 11.7   | н      | Н                  | Н   | Н       | Ч  | 11.4  | 11.4               |
| 800                 | 1726               | 247        | 37                 | 28                | 9    | 24     | 19     | 17       | 17     | 217                | ın     | 213.5              | m      | ന                  | 207        | 90                 | 204.5         | 203    | 203                | 9  | 201.5  | 8      | 8                  | 199 | 199     | 97 | 196.5 | 9                  |
|                     | , <sub>1</sub>     | <b>7</b> 6 | 4                  | ιυ                | 9    | 7      | 8      | σ        | 10     | 11                 | 12     | 13                 | 14     | 15                 | 16         | 17                 | 18            | 19     | 20                 | 21 | 22     | 23     | 24                 | 25  | 26      | 27 | 28    | 29                 |

RESULT

| probable proline-r<br>hich molecular mas | hydroxyproline-ric | hypothetical prote | hypothetical prote | calphotin - fruit | extensin-like prot | probable serine/th | probable proteinas | cell wall glycopro | proline-rich prote | hypothetical diver | proline-rich prote | US4 protein - huma | C-terminal domain- | hydroxyproline-ric | 7. |
|------------------------------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----|
| F84522<br>T18535                         | 506733             | T04455             | E86255             | A47283            | T11671             | T36729             | G70597             | S08314             | B24264             | T38459             | T17547             | C43674             | T31420             | S22456             |    |
| 2 0                                      | 1 (1               | ~                  | Ŋ                  | N                 | ď                  | 7                  | 7                  | N                  | 7                  | N                  | ~                  | ~                  | 7                  | 7                  |    |
| 191                                      | 620                | 731                | 744                | 873               | 280                | 576                | 550                | 267                | 240                | 1794               | 544                | 669                | 1268               | 350                |    |
| 11.2                                     | 11.2               | 11.2               | 11.2               | 11.2              | 11.1               | 11.1               | 11.0               | 11.0               | 11.0               | 11.0               | 10.9               | 10.9               | 10.9               | 10.8               |    |
|                                          |                    | S                  | Ŋ                  | 'n                | ι                  | 91                 | 190                | 189.5              | 83                 | 89                 | 88                 | 88                 | 188                | .87                |    |
| 194<br>193 5                             | 193                | 192.5              | 192.               | 192               | 191                | П                  |                    | 18                 | _                  | -                  | -                  | -                  | -                  | m                  |    |

# ALIGNMENTS

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1395

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1396 ---APPAPAPSSGGYSG-GSSGGS-------AAGGGGGGSSGGYSGGSAAPP 1434
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                                                                                                                                 113 IDNPVGGFSFALPAGWVESDAAHFDYGSALLSKTTGDPPFFGQPPPVANDTRIVLGRLDQ 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233 KPNGQIWIGVIGSPAANAPDAGPPQRWFVVWLGTANNPVDKGAAKA----LAESIRPLVA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PADPNA-PPPVIAPNAPQPVRIDNPVGGFSFALPAGWVESDAAHFDYGSALLSKTTGDP 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cispecies: Zea mays (maize)
Cispecies: Zea: Zea mays (maize)
Risubinstein, A.L.; Broadwater, A.H.; Lowrey, K.; Bedinger, P.A.
Submitted to the RMBL Data Library, June 1994
Aipescription: Pex genes: pollen-specific genes with extensin-like domains.
Aireference number: S49915
                                                                                                                                                                                                                  569 PAPVASPPPVKSPPPTLVASPPPPVKSPPPPA-PVASPPPVKSPP---PPTPVASPP
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                                                                                                                                                                                                                                                                                                       173 KLYASAEATDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFSDPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1435 PP-----PPAPAPAPAPSSGGYSG--GSSGGSAAGGGGSSGGYTGGSAAP---
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-1188 «KUB>
A,Cross-references: EMBL:Z34465; NID:g600117; PIDN:CAA84230.1; PID:g600118
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                                                                                                                                                                                                                  1351 SGGYSGGSSGGSAÄGGGGGSSGGYTGGSÄ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1539 PPPPA 1543
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                                                 C. Species:

C. Sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein Y50E8A.g - Caenorhabditis elegans
C;Species: Genorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Genorhabditis elegans
C;Accession: T31611
R;Steward, C.
Submitted to the EMBL Data Library, September 1999
A;Reference number: Z21047
A;Accession: T31611
A;Accession: T31611
A;Accession: T31611
A;Accession: T31611
A;Accession: T31611
A;Accession: T3161
A;Acces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167 DNIKAAVRLGSDWGEFYLPYPGTRINQETIPLHANGIAGSASYYEVKFSDPNKPIGQICT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 PPAPATPVAPPPPAAANTPNAQPGDPNAAPPPADPNAPPPPVIAPNAPQPVRIDNPVGGF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52 APSPAQEIITPLPGAPVSSEAQPGDPNA--PSLDPNAPYPLAVDPNAG---RITNAVGGF 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SFALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPPVANDTRIVLGRLDQKLYASAEA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TDSKAAARLGSDMGEFYMPYPGTRINOETVSLDANGVSGSASYYEVKFSDPSKPNGQIWT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MHQVDPNLTRRKGRLAALAIAAMASASLVTVAVPATANADPEPAPPVPTTAASPPSTAAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 GVIGSPAANAPDAGPPORWFVVWLGTANNPVDKGAAKALAESIRPLVAPPPAAPAPA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------TAAAPPAPATPVAPPPAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 241; DB 2; Length 1585;
; Pred. No. 7.1e-06;
12; Mismatches 122; Indels 134; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56.8%; Score 980; DB 2; Length 287; 66.8%; Pred. No. 8.8e-47; Live 21; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: CESP:Y50E8A.g
A;Introns: 25/3; 60/1; 133/2; 217/3; 270/3; 337/2; 400/1; 746/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 PEPAPPVPTTAASPPS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.0%;
26.6%;
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Best Local Similarity 26.6%
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 199; Conservative
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Best Local Similarity
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13;

16

682

extensin - Volvox carteri (fragment) C,Species: Volvox carteri

-----DPNAAPPPADPNAPPPPVIAPNAPQPVR 112

76 ANTPNAQPG-

us-10-720-192-2.rpr

| CDRESSIONS SOLOGY   Secquence_revision 04-Dec-1992   Start_change 21-Jul-2000                                                                                                                     | Db 28 AASPVISTITAPPPITAAPPTTATTAPPPTTTAPPVSAAQPPASPAVIPTSPAAPPAUDRAWSABDA Db 89 AVYSSATTPPQDPRAGAPPADPAAPPPPVIABNAPQPVRIDNEWGGFSFALDAGWVEBDA Db 113 AMPDVGSALLSKITGDPPPGQPPPWARNTRIVIGRIANGSPARLDGGWASDA Db 123 | AAQPPASPVTPPPAVTPTSPPAPKV 87  QPVRIDNPVGGFSFALPAGWVESDA 133 APASPPAPARLGSDM 193 APASPPAPA 144  SDSKFNGQIWTGVIGSPAANAPDA 253  SPPDAAPVSPPVQAPSP 161  PPPAPAPAPAPAPEP 300    PPPAPAPAPAPAPE |
|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| A;Residues: 1-222 <sto> A;Cross-references: GB:AE005173; NID:g6524187; PIDN:AAF15072.1; GSPDB:GN00141 C;Genetics: A;Gene: F14K14.17 A;Map position: 1</sto>                                       | 2829 KPAA                                                                                                                                                                                                       |                                                                                                                                                                                           |
| ch 13.1%; Score 226.5; DB 2; Length 222; 1 Similarity 23.1%; Pred: No. 6.2e-06; 75; Conservative 14; Mismatches 75; Indels 161; Gaps 9; 22 AWASASLVIVAVPATANADPEPAPPPYTTAASPRAAPAPATATPVAPPPAA 75 | EPAPAPAPAGEVAPTPTPORT                                                                                                                                                                                           |                                                                                                                                                                                           |

18;

72

237

187

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hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: O3-De-1999 #sequence_revision O3-Dec-1999 #text_change 31-Mar-2000
C;Accession: F75518
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; R;White, O.; Eisen, W.; Vantathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Maß, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: F75518
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: NA
A;Molecule type: NA
A;Molecule type: NA
A;Cross-references: GB:AE001904; GB:AE000513; NID:g6458129; PIDN:AAF10038.1; PID:g645814:
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                        118 ASAPPIPGAVPSVAAPPIPNAPLSPAPAVPSIPSSSAPPIPDIPSSAAPPIPIVPSSPAP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97 APPPPV-----IAP--NAPOPVRIDNPVGGFSFALPAGWVESDAAHFDYGS---- 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFSDPSKPNGQIWTGVIGSPA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSTKIOTENHKSPSOPPLPSSAPPIPTSHAPPLPPTAPPPPSLPNVTSAPKKATSAPAPP 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---PPLPN---TTSVPPNKA 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANAPDAGPPORWFVVWLGTANNPVDKGA---AKALAESIRPLVAPPPAPAPAPAPAPA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Superfamily: herpesvirus immediate-early protein IE110; RING finger homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 PLPLSGASAPKVPQNRPHMPSVRPAHRSHQRKSSNISLPSVSAPPLPSASLPTHVSNPPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --TRIVLGRLDQKLYASAEATDSKAAA
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                             Indels 121;
                                                                                                                                                                                                                                                                 Length 817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 839;
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12.6%; Score 217.5; DB 2;
Best Local Similarity 25.4%; Pred. No. 7.1e-05;
Matches 95; Conservative 24; Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               353 P-----PPLPAAMSSASTNSVKATPVPPTLA----
                                                                                                                                                                                                                                                            12.6%; Score 217.5; DB 2; 26.3%; Pred. No. 6.9e-05; tive 31; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                             24 ASASLVTVAVPATA----NADPEPAPPVPT--TAASPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 ----ALLSKITGDPPFPGQPPVAND----
                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 P----AAANTPNAQPGDPNAAP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            304 PAPAGEVAPTPTTP 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            452
               F)372-382/Region: proline-rich
F)396-406/Region: proline-rich
F)421-445/Region: proline-rich
F)518-528/Region: proline-rich
F)567-577/Region: proline-rich
F)608-621/Region: proline-rich
F)679-661/Region: proline-rich
F)704-710/Region: proline-rich
                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 26.3$
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            441 PPP----PPTLTTNKP
proline-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: DR0458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N.Alternate names: prolin-rich protein VRP1; protein L8300.13; protein YLR337c C; Species: Saccharomyces cerevisiae C; Date: 23.Feb-1995 #sequence revision 11-Aug-1995 #text_change 23-Mar-2001 C; Accession: S51342; S39626; S57435 R; Du, Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21
                                                                    Species: Mycobacterium leprae
| Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MHQVDPNLTRRKGRLAALA I AAMASASLVTVAVPATANADPEPAPPVPTTAAS PPSTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-162,'F',164-817 <MUN>
A;Cross-references: EMBL:X87806; NID:g871534; PID:g871535
A;Experimental source: strain W303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ribu, Z. submitted to the EMBL Data Library, December 1994 A;Description: The sequence of S. cerevisiae cosmid 8300. A;Reference number: S51339 A;Recession: S51342
                                             [imported] - Mycobacterium leprae (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                  12.7%; Score 219.5; DB 2; 52.1%; Pred. No. 5.7e-06; iive 8; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APSPAQEIITPLPGAPVSSEAQPGDPNA--PSLDPN 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 PPAPATPVAPPPPAAANTPNAQPGDPNAAPPPADPN 96
                                                                                                           C, Accession: T44744

R: Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, October 1997
A; Reference number: 222833
A; Accession: T44744
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Moulecule type: DNA
A; Residues: 1-85 < PAR>
                                                                                                                                                                                                                                                                                                             Cross-references: EMBL:AL008609; PIDN:CAA15433.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: SGD:VRP1; MDP5; END5
A;Cross-references: SGD:SO004329; MIPS:YLR337c
A;Map position: 12R
F:514/Region: proline-rich
F;77-85/Region: proline-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  verprolin - yeast (Saccharomyces cerevisiae)
                                                                                                                                                                                                                                                                                                                                    A, Experimental source: cosmid B1788 C, Genetics: A, Note: 43L
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 52.18
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Filt-180/Region: proline-rich
F;216-245/Region: proline-rich
F;305-336/Region: proline-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-817 <DUZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
                                                antigen 43L
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17; 70 22 AMASASLVIVAVPATANAD----PEPAP--PVPITAASPPSTAAAP----PAPATPVAP-Indels 131; Gaps

| Oy 239 WIGUIGS                                                      | Oy 316 TPTP 319  Db 795 PVNP 798  RESULT 13  T06291  extensin homolog T9E8.80 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-Jun-1999 C;Accession: T06291 C;Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Schuell submitted to the Protein Sequence Database, April 1999 A;Reference number: Z15588 |
|---------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Db 91 APATKPEPPRAKATDAREPROPERPEPERPEPERPEPERPREPREPREPREPREPREPREP | 254 AS<br>115 NP<br>311 DS<br>150 -P<br>371 TT<br>197 YM<br>427 -T                                                                                                                                                                                                                                                                                                                                                                 |

| A) SCROSS = references: BMBL-ALO49608 A) Experimental sources: cultivar Columbia, BAC clone T988 C) Genetics: A) Motes T988 C) Conservative 20; Mismatches 107, Indels 119, Gags 13, Observative 26; Mismatches 107, Indels 119, Gags 113, Observative 26; Mismatches 107, Indels 119, Gags 113, Observative 26; Mismatches 107, Indels 119, Gags 113, Observative 26; Mismatches 26; Mismatches 27, Observative 27, Observ | 2913                                              |
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| 64;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 252 DAGPPQ<br>     <br>  135 PATPP-<br>306 PAG 30 |
| 10 RRKGRLAALAIAAMASASLVTVAVP<br>2683 RRHRRARSLAALATOGWRPPALPDTVAPP<br>62PAPATPVAP-PPPAAANTPNAQP<br>2742 LPLGPQAAGQASPALPIDPVPPPVATGTVLP<br>111 VRIDNPVGGFSPALPAGWVESDAAHFDYGSALL<br>12800 -RLTRPAVASL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | Cy 306 PAG 308                                    |

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GenCore version 5.1.6
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OM protein - protein search, using sw model

July 7, 2004, 18:17:39; Search time 10.5 Seconds (without alignments) 1611.695 Million cell updates/sec Run on:

US-10-720-192-2 1726 1 MHQVDPNLTRRKGRLAALAL......PAGEVAPIPTIPTPQRTLPA 325 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description    | Q50906 mycobacteri | mycobac |     |     | Q9fpg6 chlamydomon | sacchar | herpe | homo sa | xenor |       |      |       |     |     | Q9jka7 rattus norv | Q9r0i7 mus musculu |       | sch: |      | homo s | herpe | рошо  | homo | streg |      | homo  | strep |      |     | P05142 mus musculu |     | drosophil | P48634 homo sapien |
|-----------|----------------|--------------------|---------|-----|-----|--------------------|---------|-------|---------|-------|-------|------|-------|-----|-----|--------------------|--------------------|-------|------|------|--------|-------|-------|------|-------|------|-------|-------|------|-----|--------------------|-----|-----------|--------------------|
| SUMMARIES | DB ID          |                    |         |     |     | GP1                |         | TEG   |         | XP2   |       | _    | CPN   |     |     | 1 HCN4_RAT         |                    |       |      | SHK  |        |       | _     |      | IF2   |      |       | IF2   |      | CSP |                    | APG | OSAL      | 1 BATZ_HUMAN       |
|           | Length D       | 325                | 325     | 381 | 287 | 555                | 817     | 3164  | 1083    | 439   | 802   | 3421 | 865   | 283 | 620 | 1198               | 1386               | 267   | 1794 | 2167 | 2715   | 669   | 5179  | 331  | 1033  | 1300 | 639   | 1046  | 1271 | 347 | 261                | 534 | 2716      | 2142               |
| ð         | Query<br>Match | 100.0              | 99.7    |     |     |                    |         |       |         |       | 11.9  |      |       |     |     | 11.2               |                    | ٠     |      |      | •      | •     |       |      | •     |      |       |       |      | •   |                    |     |           | 4                  |
|           | Score          | 17                 | 1720    | 985 | 980 | (1)                | 217.5   | 13    | 210     | N     | 205.5 | 0    | 197.5 | 197 | 193 | 192.5              | -                  | 189.5 | 189  | М    | 188.5  | Н     | 186.5 | 186  | Н     | 85   | 184.5 | 84    | 184  | 183 | 182                | 80  | 180.5     | 73                 |
|           | Result<br>No.  |                    | 73      | m   | 4   | ß                  | 9       | 7     | 80      | σ     | 10    | 11   | . 12  | 13  | 14  | 15                 | 16                 | 17    | 18   | 19   | 20     | 21    | 22    | 23   | 24    | 25   | 26    | 27    | 28   | 59  | 30                 | 31  | 32        | 33                 |

| P06915 plasmodium |            |            |            |            |            |            |            |            |            |            |            |
|-------------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| CSP PLABE         | CM32_HUMAN | SYJ1_HUMAN | DIA1 HUMAN | SHK1 HUMAN | TRX2 MOUSE | BAT3 HUMAN | PMP3 MOUSE | WASP HUMAN | SF01 HUMAN | IRS2_HUMAN | NCR2_HUMAN |
| .,                | -          | Н          | Н          | н          | Н          | Н          | Н          | н          | Н          | Н          | -          |
| 339               | 245        | 1575       | 1248       | 2161       | 290        | 1132       | 296        | 502        | 639        | 1324       | 2517       |
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| 10.4              | 10.3       | 10.3       | 10.3       | 10.3       | 10.2       | 10.2       | 10.1       | 10.1       | 10.1       | 10.1       | 10.1       |
| 179 10.4          | •          | •          |            | • •        |            |            | •          |            |            | •          |            |

## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 40-49, AND CHARACTERIZATION OF CARBOHYDRATE-LINKAGE SITES BY MASS SPECTROMETRY.
STRAIN-H37RV;
MEDLINE-2001139; Pubmed-10542234;
Medline-2001139; Pubmed-10542234;
Barzu O., Mamane A., Pescher P., Riviere M., Romain F., Puzo G.,
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                                                                       Nagai S., Wiker H.G., Harboe M., Kinomoto M.; "Isolation and partial characterization of major protein antigens in the culture fluid of Mycobacterium tuberculosis.";
                                                                                                                                                                                                                                                                                                    PARTIAL SEQUENCE, AND CARROHYDRAIE-LINKAGE SITES.
MEDLINE=96196153; PubMed=8626314;
Dobos K.M., Khoo K.H., Swiderek K.M., Brennan P.J., Belisle J.T.;
"Definition of the full extent of glycosylation of the 45-kilodalton Jlycoprotein of Mycobacterium tuberculosis.";
J. Bacteriol. 178:2498-2506(1996).
                                                                                                                                                                                    MEDLINE=95347792; PubMed=762204;
Dobos K.M., Swiderek K., Khoo K.-H., Brennan P.J., Belisle J.T.;
Modence for glycosylation sites on the 45-kilodalton glycoprotein whycobacterium tuberculosis ";
Infect. Immun. 63:2846-2853(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BIOTECHNOLOGY: Major immunodominant antigen that has potential a vaccine against tuberculosis. APA-ELISA could be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISCELLANDOUS: Changes in the mannosylation pattern of this protein affect its ability to stimulate T-lymphocyte response. CAUTION: Was originally thought to be involved in molybdenum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Decreased capacity of recombinant 45/47-kDa molecules (Apa) of Mycobacterium tuberculosis to stimulate T lymphocyte responses Mycobacterium tuberculosis to stimulate T lymphocyte responses trelated to changes in their mannosylation pattern."; J. Biol. Chem. 274:32023-32030(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X80268; CAA56555.1; -.
EMBL; X89258; CAA67645.1; -.
EMBL; Z83859; CAA67645.1; -.
EMBL; AE007048; AAK46179.1; -.
ENRL; AE007066; D70666.
TICR; MT1908; -.
TUBerculist; Rv1860; -.
Antigen; Glycoprotein; Repeat; Signal; Complete proteome. SIGNAL
40 325 ALANINE AND PROLINE-RICH SEC
                                      PARTIAL SEQUENCE, AND CHARACTERIZATION.
                                                                                                                                                                          PARTIAL SEQUENCE, AND GLYCOSYLATION.
                                                           PubMed=1898899;
Bacteriol. 184:5479-5490(2002)
                                                                                                                                   Infect. Immun. 59:372-382(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY MASS SPECTROMETRY.
STRAIN=H37Rv;
                                                           MEDLINE=91099989;
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MEDLINE=22709107; PubMed=12788972;
MEDLINE=22709107; PubMed=12788972;

Rarnier T. Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,

Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,

Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,

Parkhill J., Barrell B.G., Colle S.T., Gordon S.V., Hewinson R.G.;

"The complete genome sequence of Mycobacterium bovis.";

Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhao W., Schorey J.S., Bong-Mastek M., Brown E.J., Ratliff T.L.; "Identification, sequence and characterization of the M. bovis BCG
                                                                                                                                                                                                                                                                                                                                                  .0
                                                                                                                                                                                                                                                                                                100.0%; Score 1726; DB 1; Length 325; 100.0%; Pred. No. 1.5e-80;
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Corynebacterineae, Mycobacteriaceae, Mycobacterium.
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Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases
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59E5D0455A997BED CRC64;
                                                                                                                                     (MAN. . .).
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(MAN).
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30-MAY-2000 (Rel. 39, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Alanine and proline-rich secreted protein apa p
APA OR MB1891.
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(Fibronectin attachment protein) (FAP-
APA OR MODD OR ML2055 OR MLCB1788.01C.
Mycobacterium leprae.
                                                                    Mol. Microbiol. 21:321-329(1996).
-!- SUBCELLULAR LOCATION: Secreted.
 MEDLINE=97011577; PubMed=8858587;
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MEDLINE=94086110; PubMed=8262636;
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                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the buropean Bloinformatics Institute. There are one restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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30-MAY-2000 (Rel. 39, Last sequence update)
36-PEDB-2003 (Rel. 41, Last annotation update)
Alanine and proline-rich secreted protein apa precursor (45/47 kDa antigen) (Fibronectin attachment protein) (FAP-A).
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBL_TaxID=1764;
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                                                                                                                                                                     Antigen; Glycoprotein; Repeat; Signal; Complete proteome SIGNAL 1 39 BY SIMILARITY.
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Pred. No. 3e-80;
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SUBCELLULAR LOCATION: Secreted
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EMBL; BX248340; CAD94594.1; -.
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325 AA;
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STRAIN=101;
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Q48<u>9</u>19;
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Schorey J.S., Holsti M.A., Ratliff T.L., Allen P.M., Brown E.J., "Characterization of the fibronectin-attachment protein of Mycobacterium avium reveals a fibronectin-binding motif conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84;
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.1%; Score 985; DB 1; Length 38 ilarity 55.2%; Pred. No. 2.7e-43; Conservative 27; Mismatches 66; Indels
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ALANINE AND PROLINE-RICH SECRETED PROTEIN
                                                                                                                                                                                                                     "A Mycobacterium leprae gene encoding a fibronectin binding protein is used for efficient invasion of epithelial cells and Schwann cells."; Infect. Immun. 63:2652-2657(1995).
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                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-95310024; PubMed=7790081;
Schorey J.S., Li Q., McCourt D.W., Bong-Mastek M., Clark-Curtiss J.E.,
Ratliff T.L., Brown E.J.;
                                                                                                                                                                                                                                                                                                                             STRAIN=TN;
MEDLINB=21128732; PubMed=11234002;
MEDLINB=21128732; PubMed=11234002;
Wheeler P. R., Horner N., Farkhill J., James K.D., Thomson N.R., Wheeler P. R., Horner N., Garnier T., Churcher C., Harris D., Mungall K., Bebham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Ruthert S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Barrell B.G.;
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                                                     the
Wieles B., van Agterveld M., Janson A., Clark-Curtiss J.E.,
Rinke de Wit T.F., Harboe M., Thole J.;
"Characterization of a Mycobacterium leprae antigen related to
secreted Mycobacterium tuberculosis protein MPT32.";
Infect. Immun. 62:252-258(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 980; DB 1; Length 287; Pred. No. 3.7e-43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
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SIGNAL 1 39 POTENTIAL.
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EMBL; ALS83924; CAC31010.1; -.
EMBL; AL008609; CAA15433.1; -.
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Best Local Similarity 66.8<sup>†</sup>
Matches 199; Conservative
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oma; ML2055; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96
                                                                                            227 SVVGSPAASTPDVGPSQRWFVVWLGTSNNPVDKGAAKELAESIRSEMAPIPASVSAPA 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycosylated polyproline II rods-with-kinks as a structural motif in lant hydroxyproline-rich glycoproteins."; iochemistry 40:2978-2987(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 ADPEPAPVPTTAASPPSTAAAPPAATPV--APPPPAAANTPNAQPGDPNAAPPPADPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-91017504; PubMed=1699225;
Adair W.S., Apt K.E.;
"Cell wall regeneration in Chlamydomonas: accumulation of mRNAs encoding cell wall hydroxyproline-rich 91ycoproteins.";
Proc. Natl. Acad. Sci. U.S.A. 87:7355-7359(1990).
-:- FUNCTION: Major component of the outer cell wall W6 (crystalline)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 124; Gaps
Chlamydomonas reinhardtii.
Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
Chlamydomonadaceae, Chlamydomonas.
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VEGETATIVE CELL WALL PROTEIN GPI.
VEGETATIVE CELL WALL PROTEIN GPI.
POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ferris P.J., Woessner J.P., Waffenschmidt S., Kilz S., Drees J.,
Goodenough U.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vegetative cell wall protein gpl precursor (Hydroxyproline-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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-!- PIM: N-glycosylated and O-glycosylated.
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PRINTS; PR01218; PSTLEXTENSIN.
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GlycoSuiteDB; Q9FPQ6; -.
                                                                                                                                                                                                                                                                                                                                                            GP1 CHLRE
Q9FPG6; Q03927;
28-FB3-2003 (Rel. 41, Created)
28-FB3-2003 (Rel. 41, Last seqn
28-FB3-2003 (Rel. 41, Last seqn
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GP1.
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STRAIN=S2886 / AB972;

MEDLINE=97313267, PubMed=9169871;

A MEDLINE=97313267, PubMed=9169871;

A Beneson M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W., Dohnston M., Hillier M., Coffeau A., Hebling U., Heumann K., A Heuss-Neitzel D., Hilbert H., Miger F., Kleine K., Koetter P., Louis B.J., Messenguy F., Mewes H.-W., Micsga T., Moestl D., A Mueller-Auer S., Nerwich U., Poermains B., Rieger M., Rinke M., Rose M., Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Schertens B., Scholler P., Schwager C., Schwarz S., A Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhasselt P., Vierendeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E., Wenture 387:87-90(1997).

Inture 387:87-90(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                     276
                                                                                                                  --- 329
--NTPMPPSPPSP 293
                              PPVANDTRIVLGRLDQKLYASAEATDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANG
                                                                                     217 VSGSASYYEVKFSDPSKPNGQIWTGVIGSPAANAPDAGPPQRWFVVWLGTANNPVDKGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Involved in cytoskeletal organization and cellular growth. May exert its effects on the cytoskeleton directly, or indirectly via proline-binding proteins (e.g. profilin) or
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SGD; S0004329; VRP1.
GO; GO:0005857; C:actin cortical patch (sensu Saccharomyces); IDA.
                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95058201; PubMed=7968536;
Donnelly S.F.H., Pocklington M.J.; Pallota D., Orr E.;
"A proline-rich protein, verprolin, involved in cytoskeletal organization and cellular growth in the yeast Saccharomyces
                                                                                                                                                            277 KALAESIRPLVAPPAAPAPAPAPAPAPAPAPAGEVAPTPT-TPTP
                                                                                                                VRP1_YEAST STANDARD; PRT; 817 AA. P37370; Q06133; Cl-OCT-1994 (Rel. 30, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                  OR MDP2 OR END5 OR YLR337W OR L8300.13.
 APPPPSPPPPPP----PFPA-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mol. Microbiol. 10:585-596(1993)
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                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4932;
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                                                        294 PP.
                                                                                                                                                                                                                                                                                                                    Verprolin.
VRP1 OR MD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97 APPPPV-----IAP--NAPOPVRIDNPVGGFSFALPAGWVESDAAHFDYGS---- 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 -----ALLSKTTGDPPFPGQPPVAND-----TRIVLGRLDQKLYASAEATDSKAAA 187
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                                                                                                                                                                                                                                                                                                                                                                                      DVGRYTIGGSNSIVGAKŠGNERIVIDDSRFKWTNVSQMPKP
RPFQNKTKLYPSGKGSSVPLDLTLFT -> HLRWIPVPLIA
PVKTLNNGYFLQVDRRCNTSIIRIQINQMLM (IN REF.
                                                                                                                                                                                                                                                                                                                                                                  PSTMDTGTSNSPSKNLKQRLFSTGGSTLQHKHNTHTNQPDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          293 SSTKIQTENHKSPSQPPLPSSAPPIPTSHAPPLPPTAPPPPSLPNVTSAPKKATSAPAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 ASASLVTVAVPATA-----NADPEPAPPVPT--TAASPP----STAAAPPAPATPVAPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 RLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFSDPSKPNGQIWTGVIGSPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              353 P-----PPLPAAMSSASTNSVKATPVPPTLA-----PPLPN---TTSVPPNKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248 ANAPDAGPPORWFVVWLGTANNPVDKGA---AKALAESIRPLVAPPPAPAPAPAPAP-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 817;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRC64;
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
GO; GO:0003779; F:actin binding; IDA.
GO; GO:0007015; P:actin filament organization; IPI.
GO; GO:0007015; P:actin filament organization; IPI.
GO; GO:0007121; P:polar budding; IMP.
GO; GO:0006970; P:response to osmotic stress; IMP.
InterPro; IPR003124; WH2.
SMART; SM00246; WH2; 2.
Cytoskeleton; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.6%; Score 217.5; DB 1; 26.3%; Pred. No. 0.00018; ive 31; Mismatches 125;
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R (IN REF. 1).
E (IN REF. 1).
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01-MAR-1989 (Rel. 10, Last sequence update)
01-BR-1993 (Rel. 25, Last annotation update)
Large tegument protein (Virion protein UL36).
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POLY-PRO.
POLY-PRO.
POLY-SER.
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Alphaherpesvirinae; Simplexvirus.
NCBI_TAXID=10299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82593 MW;
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                                                                                                                                                                                            245
3357
406
431
468
708
308
350
689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 817 AA;
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P10220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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TEGU HSV11
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SUBCELLULAR LOCATION: Nuclear
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                             15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2742 LPLGPQAAGQASPALPIDPVPPPVATGT--VLPGGENRRPPLTSGPAPTPPRVPVGGPQR 2799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----AVASLSESRESLPSPWDP---ADPTAPVLGR- 2832
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 RRKGRLAALAIAAMASA-----SLVTVAVPATANADPEPAPPVPTTAASPPSTAAAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------PAPATPVAP-PPPAANTPNAQPGDPNAAPPPADPNAPPPVIAPNAPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VRIDNPVGGFSFALPAGWVESDAAHFDYGSALLSKTTGDPFFPGQPPPVANDTRIVLGRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOKLYASAEATDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DT T213 HUMAN STANDARD; PRT; 1083 AA.

AC 000268; 099721; 09BR40; 09BX42;

T 15-JUL-1998 (Rel. 36, Last sequence update)

T 15-JUL-1998 (Rel. 34), Last sequence update)

T 15-MAR-2004 (Rel. 43, Last annotation update)

T Transcription initiation factor TPIID 135 kDa subunit (TAFII-135)

T TAFII135) (TAFII-130) (TAFIII-130).

T TAFA OR TAFAA OR TAF2CI OR TAF2CI OR TAFIII30.

Homo sapiens (Human).

C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; N Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

X NBI TAXID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                12.4%; Score 213.5; DB 1; Length 3164; 26.5%; Pred. No. 0.001; cive 17; Mismatches 117; Indels 119; Gaps
SEQUENCE FROM N.A.
MEDLINE-88274327; PubMed=2839594;
MCGEOCH D.J., Dalrymple M.A., Davison A.J., Dolan A., Frame M.C.,
MCNab D., Perry L.J., Scott J.B., Taylor P.;
"The complete DNA sequence of the long unique region in the genome
                                                                   herpes simplex virus type 1.";
J. Gen. Virol. 69:1531-1574(1988).
-!- FUNCTION: Tegument protein.
-!- SIMILARITY: BELOWGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36,
EHV-1 24, EBV BPLF1, HVS-1 64, VZV 22, AND HCMV UL48.
                                                                                                                                                                                                                                                                                                                                                                                               Length 3164;
                                                                                                                                                                                                                                                                                                                                                        2911 2980 35 X 2 AA TANDEM REPEATS OF P-Q. 3164 AA; 335857 MW; CC5D31FF4F9FB3F4 CRC64;
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                                                                                                                                                                                                                                                          EMBL, X14112, CAA32311.1; -.
PIR, 130085, WMBEH6.
InterPro; IPR006928; Herpes teg N.
InterPro; IPR005210; Herpes_UL36.
Pfam; PF04843; Herpes_Eg N; 1.
Pfam; PF03586; Herpes_UL36; 1.
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Best Local
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ID T2D3_HH
DT_129_HH
DT_15-UUL.
DT_15-UUL.
DT_15-UUL.
DT_15-UUL.
DE TAFIII
GN TAFIII
GN TAFIII
OC HUMC SE
OC BUKATY
OC MAMMAL.
OC NORDITI
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REAL GESTER DAY. 11:1381-1393(1997).

REAL GESTER DAY. 11:1381-1393(1997).

REAL GESTER DAY. 11:1381-1393(1997).

REAL GESTER DAY BOUNDED THE SET OF THE SEQUENCE FROM N.A. THE SEQUENCE FROM N. Matthews D.H., Ashurst J., Barbage A.K., Bagguley C.L., RA Deloukas P., Matthews D.H., Bartes K.N., Beare D.M., Bearley J., Barlow K.F., Blakes K.N., Beare D.M., Bearley J., Barlow K.F., Blakes S.E., Carder C., Carter N.P., RA Beasley O.P., Bird C.P., Blakes S.E., Carder C., Carter N.P., Collson A.C., Clarm M., Clark G., Clark G., Clark G., Clark S.Y., Clee C.M., Collson A.G., Frankland R.E., Comnor R.E., Corby N.R., RA Clegg S., Cobley V.E., Collier R.E., Comnor R.E., Corby N.R., R. Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.J., RA Frankland J.A., Fraser A., French L., Garner P.J., RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., RA Lebvaselaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D., RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., Dannson D., RA Marker R., Share S., Mistry D., Moore M.J.F., Pearce T.A. V., Deck A.I., Pearlel R., Share C.M., Solarlund C., Steward C.A., Sollston J.E., Allacop A., Tromans A.C., Vaudin M., Wallay N., Willies S.A., Tromans A.C., Whiley D.L., Williams S.A., Mistries P. Williams B. Williams S.A., Mistries P. Williams B. Williams S.A., Mistries P. Williams D.L., Williams C., Williams D.L., Williams C., Williams C., Williams C., Williams C., Williams C., Williams D.L., Williams C., Williams D.L., Williams C., Williams D.L., Williams C., Williams C. W., Beck S., R. R. R. Mistries A. Mistries A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mol. Ceil. Biol. 20:340-351(2000).

-!- FUNCTION: Makes part of TRIID is a multimeric protein complex that plays a central role in mediating promoter responses to various activators and repressors. Potentiates transcriptional activation by the AF-2S of the retinoic acid, vitamin D3 and thyroid hormone.
-!- SUBINIT: TFIID is composed of TATA binding protein (TBP) and a number of TBP-associated factors (TAFS). Component of the TFTC-HAT composed of TAFSL, TAFSL, TAPSL, SUBT31/SPT3, TAFZ/TAFIII50, TAF4/TAFII135, TAF5/TAFII100, GCN5L2/GCN5, TAF10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Davidson I.;
"The human TFIID components TAP(II)135 and TAF(II)20 and the yeast
SAGA components ADA1 and TAF(II)68 heterodimerize to form histone-like
                                  Mengus G., May M., Carre L., Chambon P., Davidson I., "Human TAF(II)135 potentiates transcriptional activation by the AF-2s of the retinoic acid, vitamin D3, and thyroid hormone receptors in mammalian cells ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              identification in The Tetc-Hat COMPLEX WITH TAF5L; TAF6L; TADA3L; SUFT3H; TAF2; TAF5; TRRAP; GCN5L2 AND TAF10.
MEDLINE=99303588; Pubmed=10373431;
Brand M., Yamamoto K., Staub A., Tora L.;
"Identification of TATA-binding protein-free TAFII-containing complex subunits suggests a role in nucleosome acetylation and signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence and comparative analysis of human chromosome 20.";
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human TFIID
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Gangloff Y.-G., Werten S., Romier C., Carre L., Poch O., Moras D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 870-918 IN COMPLEX WITH
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Tanese N., Saluja D., Vassallo M.F., Chen J.-L., Admon , Molecular cloning and analysis of two subunits of the ecomplex: hTAFIL130 and hTAFIL100.";
Proc. Natl. Acad. Sci. U.S.A. 93:13611-13616 (1996).
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WEDLINE=97336072; PubMed=9192867;
                                                                                                                                                                                                                                                      Genes Dev. 11:1381-1395(1997).
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                                                                                                                                                                                                                    mammalian cells.
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                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 DSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFSDPSKP----NGQ 237
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                                                                                                                                                                                             GO; GO:0005669; C:transcription factor TFIID complex, TAS.
GO; GO:0016251; F:general RNA polymerase II transcription fac.
GO; GO:0005515; F:protein binding; TAS.
GO:0003713; F:transcription co-activator activity; TAS.
InterPro; IPR007900; TAF4.
InterPro; IPR003894; TAF hom.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92;
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POLY-HIS.
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POLY-SALA.
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POLY-REP. 3).
G -> GPG (IN REF. 2).
G -> GPG (IN REF. 2).
G -> GPG (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.2%; Score 210; DB 1; Length 1083; 27.8%; Pred. No. 0.00056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 P -> L (IN REF. 3).
109943 MW; A6453827572A0752 CRC64;
                                                                                                                                                                                                                                                                                 regulation, Nuclear protein; 3D-structure.
0 682 TAFH/NHR1.
SIMILARITY: BELONGS TO THE TAF2C FAMILY. SIMILARITY: Contains 1 TAFH/NHR1 domain.
                                                                                                             EMBL, Y11354; CAA72189.1; -.
EMBL, AL13707; CAC36066.1; -.
EMBL, AL109911; CAC22312.2; -.
EMBL, U75308; AAC50901.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                      PDB; 1H3O; 26-SEP-02.
TRANSFAC; T02328; -.
Genew; HGNC:11537; TAF4.
                                                                                                                                                                                                                                                           Pfam; PF05236; TAF4; 1.
SMART; SM00549; TAFH; 1.
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1083 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i-SIMILARITY: Contains 2 P-type (trefoil) domains.
-i-CAUTION: Ref.2 sequence differs from that shown from position 392 onward and is shorter (418 AA) due to a frameshift.
                                                                                                                                                                                                                                                                                                                                                                                             potential growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKIN SECRETORY PROTEIN XP2.
PYRROLIDONE CARBOXYLIC ACID (PROBABLE)
33 X REPEATS OF G-[GE]-[AP] (2,4)-A-E.
XP2 XENLA STANDARD; PRT; 439 AA.
P17437; Q08944;
D1-A07-1990 (Rel. 15, Created)
01-PFB-1995 (Rel. 31, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
Xkin secretory protein xP2 precursor (APEG protein).
Xenopus laevis (African clawed frog).
Xenopus laevis (African Clawed frog).
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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PROSITE; PS00025; P_TREFOIL; 2.
Signal; Growth factor; Alternative splicing; Repeat; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                   6
                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-25 AND 344-439 FROM N.A. (ISOFORM 2) MEDLINE-92332564; PubMed=1629230; Hauser F., Roeben C., Hoffmann W.; Wars, and we member of the P-domain peptide family factors, is synthesized in Xenopus laevis skin."; J. Biol. Chem. 267:14451-14455 (1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=2;
Name=1; Synonyms=APEG;
IsoId=P17437-1; Sequence=Displayed;
Name=2; Synonyms=XP2;
IsoId=P17437-2; Sequence=VSP_004652;
-1 TISSIE SPECIFICITY: Skin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
SKIN SECRETORY P
PYRROLIDONE CARB
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P-TYPE 2.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 3-439 FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M90095; AAAS0001.1; -.
EMBL; X51394; CAA35759.1; ALT_FRAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A37331, A37331.
PIR; S07498; SKXLAG.
HSSP; P041S5; 1PS2.
InterPro; IPR000519; Ptrefoil.
Pfam; PF00088; trefoil; 2.
PRINIS; PR00680; PTREFOIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22
439
23
343
391
377
                                                                                                                                                                                                                                                            NCBI_TaxID=8355;
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protein;
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   16;
                                                                                                                                                               104
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                                                                                                                                                                                                                                                                  245
                                                                                                                                                                                                                                              EAPAP-----AEGEAPAPAFGEAPAPAFGEAPAPAP-------AEGEAPAPAP 201
                                                                                                                                                                                                                                                                                                        PA-----ANAPDAGPPQRWFVVWLGTANNPV---DKGAAKALAESIRPLVAPPPAPAPAP 297
                                                                                                                                                                                                                                                                                                                           PAPAPAEGEAPAPAPAE-----GEAPAPAPAEGEAPAPAPAEGEAPAPAEGEAPAPAEGEAPAPA 301
                                                                                                                                           82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gertler F.B., Niebuhr K., Reinhard M., Wehland J., Soriano P., "Mena, a relative of VASP and Drosophila Enabled, is implicated in the control of microfilament dynamics.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORMS 2; 3; 4 AND 5), FUNCTION, AND SUBCELLULAR
                                                                                                                                                                                                                                                                                     202 AE-----GEAPAPAPAREGEAPAPARGEAPAPARGEAPAPARGEAPAPARGE-----A
                                                                                                                                            PATANADPE-PAP-----PVPTTAASP-PSTAAAP-PAPATPVAP-PPPAAANTPNAQ
                                                                                                                                                               PAPAPAEGEAPAPAEGGAPAPAEGAEPAPADGGAPAPAPAEGGAPAPAEGGAPAPA
                                                                                                                                                                                   PGDPNA-----PVGGFSFALPAGWV
                                                                                                                                                                                                ESDAAHFDYGSALLSKTTGDPPFP----GQPPPVANDTRIVLGRLDQKLYASAEATDSKA
                                                                                                                                                                                                                                                                  AARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFSDPSKPNGQIWTGVIGS
                                                                                                                                                                                                                                                                                                                                                                                                                    ENAH MOUSE STANDARD, PRT; 802 AA.

Q03173; P70431; P70432; P70433;
01-0CT-1996 (Rel. 34, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Enabled protein homolog (NPC derived proline-rich protein 1) (NDPP-1).

Mus musculus (Mouse)
                                                                                                                       80; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sazuka T., Tomooka Y., Kathju S., Ikawa Y., Noda M., Kumar S.; "Identification of a developmentally regulated gene in the mouse central nervous system which encodes a novel proline rich protein."; Biochim. Biophys. Acta 1132:240-248(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99166867; PubMed=10069337;
Lanier L.M., Gates M.A., Witke W., Menzies A.S., Wehman A.M.,
                                                                                                    Length 439;
                                                                                                  12.0%; Score 207; DB 1; Length 43 29.2%; Pred. No. 0.00035; tive 21; Mismatches 132; Indels
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
Missing (in isoform 2).
/FIId-VSP 004652.
H -> S (IM REF. 2).
C -> W (IN REF. 2).
W, 38C4A4B57CBAE778 CRC64;
                                                                                                                                                                                                                                                                                                                                                 298 AE-PAPAPAGEVAPTPTTPQRTLPA 325
                                                                                                                                                                                                                                                                                                                                                                     AEGEAPAPAPAGGAPSPAEGGAPAAPA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93041923; PubMed=1420303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97015079; PubMed=8861907;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE=Brain;
                                                                                 41173 MW;
                                                                                                                       96; Conservative
          87:227-239(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [3]
FUNCTION, AND SUBUNIT
                                                                                439 AA;
                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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DISULFID
DISULFID
DISULFID
                                                                                                                                            34
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                                                                                                                                                                 7
                                                                                SEQUENCE
                                                                                                     Query Match
                                                            CONFLICT
                                        VARSPLIC
                                                                                                               Local
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"Mena is required for neurulation and commissure formation.";

Neuron 22:313-225(1999)

-!- FUNCTION: May be involved in microfilament assembly and cell

motility. Induces the formation of F-actin rich outgrowths in

fibroblasts. Required for neurulation and commissure formation.

-!- SUBCINIT: Binds profilin.

-!- SUBCILULAR LOCATION: Localized to focal adhesions and, to a

lesser extent, leading edges and stress fibers.

-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=3; Synonyms=Mena+;
IsoId=Q01373-4; Sequence=VSP_007259;
Name=4; Synonyms=Mena++;
IsoId=Q03173-5; Sequence=VSP_007257, VSP_007258;
-!- TISSUB SPECIFICITY: In the heart and testis and less so in the lung, skeletal muscle, kidney, pancreas and brain.
-!- SIMILARITY: Contains 1 WH1 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HLLPLPSPHLEFSLDPROKTIAFNWTCSCNCGS (in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neurogenesis; Alternative splicing.
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/FTIG=VSP_007257.
CIFC -> VFYL (in isoform 4).
/FTIG=VSP_007258.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=Q03173-2; Sequence=VSP_007255, VSP_007256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=2; Synonyms=Menā;
IsoId=203173-3; Sequence=VSP_007259, VSP_007260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO, GO:0005925; C:focal adhesion; IDA.
GO; GO:0005925; F:profilin binding; IDA.
GO; GO:0007124; F:profilin binding; IDA.
GO; GO:0007124; F:SH3-domain binding; IDA.
GO; GO:0007015; P:actin filament organization; IDA.
GO; GO:0007011; P:axor guidance; IMP.
GO; GO:0006928; P:cell motility; IDA.
GO; GO:0006928; P:cell motility; IDA.
InterPro; IPR000697; EVH1.
InterPro; IPR001960; WH1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (in isoform 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /FTId=VSP 007259.
Missing (in isoform 2)
                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      007256
                                                                                                                                                                                                                                                                                                                                                                                  Name=5; Synonyms=Mena+++;
IsoId=Q03173-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FTId=VSP
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EMBL; U72520; AACS2863.1; --
EMBL; U72521; AACS2866.1; --
EMBL; U72522; AACS2866.1; --
EMBL; U72523; AACS2866.1; --
PIR; S27200; S27200.
MGD; MGI:108360; Enah.
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                                                                                                                                                  11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            467
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                                                                                                                                                                                                                                                                    402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSASEP-----GLQAASQPAESPTPQGLVLGPPAPPPPPPPPPGGPAYASALPPPPG 566
                                                                                                                                                                                                                                                                    343 VPRPLNKNSRPSSPVNTPSSQPPAAKSCAWFISNPSPLPPSPPNISSPPGKATGPRPVL
                                                                                                                                                                                                                                                                                                                                PAAANTPNAQ----PGDPNAA-----PPPADPNAPPPPVIAPNAPQPVRIDNPVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 GFSFALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQP-PPVANDTRIVLGRLDQKLYAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 AEATDSKAAARLGSDMGEFYMPYPGTRI-----NQETVSLDANGVSGSAS---YYEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----LSHCGSQASPPPGTPLASTPSSKPSVLPSPSAGAPASAETPLNPELGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDPSKPNGQIWTGVIGSPAANAPDAGPPQRWFVVWLGTANNPVDKGAAKALAESIRPLVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOGETHER HSV-1 UL36,
                                                                                                                                                  Indels 123;
                                                                                                                                                                                                                                                                                                                                                                                      403 PVCVSSPVPOMPPSPTAPNGSLDSVTYPVSPPPTSGPAAPPPPPPPPPPPPP
                                                                                     DB 1; Length 802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 3421;
                                                                                                                                                                                                           VPATANADPEPAPPVPTTAASPPSTAAA------PPAPATPVAPPP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIR., (336'97); WZBEB6.
InterPro; IPR006928; Herpes_teg_N.
InterPro; IPR005210; Herpes_U136.
Fiam; PF04843; Herpes_teg_N.1.
Pfam; PF04843; Herpes_U136; 1.
Fiam; PF04845; Herpes_U136; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=9229566; PubMed=1318606;
Telford E.A.R., Watson M.S., McBride K., Davison A.J.;
The DNA sequence of equine herpesvirus-1.";
Virology 189:304-316 (1992).
-!- FUNCTION: Tegument protein.
-!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HS
EHV-1 24, EBV BPLF1, HVS-1 64, VZV 22, AND HCMV UL48.
/FTId=VSP_007260.
592BB975EE20F77F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---PPPAPAPABAAPAPAPAGEVAPTPTTPQRTLPA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      567 pepapanangapapapapanangapapapapapanan 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Equine herpesvirus type 1 (strain Ab4p) (EHV-1).
Viruses, dsDNA viruses, no RNA stege; Herpesviridae,
Abphaherpesvirinae; Varicellovirus.
NCBI_TaxID=31520;
                                                                                  Query Match 11.9%; Score 205.5; DB 1; Best Local Similarity 22.9%; Pred. No. 0.00072; Matches 78; Conservative 27; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 203; DB 1;
Pred. No. 0.0036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 24, Created)
(Rel. 24, Last sequence update)
(Rel. 25, Last annotation update)
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                            85844 MW;
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Best Local Similarity
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01-DEC-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                  2736 -----QPVRKSLPSQVRGGRPYIRPSLGPFKFTGPPG-----YTIPVHGLPPSDSNVT 2783
                                                                                     2564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2784 QSTKEPPK------PAVETPAAPAK-----SAAAPAAPAKSAAPAAP 2823
15;
                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Canton-S;
MEDLINE=93165729; PubMed=8094559;
Martin J.H., Benzer S., Rudnicka M., Miller C.A.;
Martin J.H., Benzer S., Rudnicka M., Miller C.A.;
"Calphotin: a Drosophila photoreceptor cell calcium-binding protein.";
Proc. Natl. Acad. Sci. U.S.A. 90:1531-1535(1993).
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                                                                                                                                                                                                                                                                                                      ------FPG-QPP----PVANDTRIV
                                                                                                                                                                                                                                                                                                                                                                                         167 LGRLDQKLYASAEATDSKAAARLGSDMGEF-YMPYPGTRINQETVSLDANGVSGSASYYE
                                                                                  2505 PTLPPKAAPLPPSDASAIMSGKPVFKYTPGNKSAVPPSVPAPPTLPPAPPLPQSTSKAAS
                                                                                                                              -----PPPVIAPNAP
                                                                                                                                                                       2565 GPPPTLPPAPPLP--OSTSKAASG----PPPTLPPAPPLPQSTSKAASGPPPTLPPAPP
                                                                                                                                                                                                                 ----SFALPAGWVESDAA---
                                                                                                                                                                                                                                                          2618 LPQSTSKAASGATQSDSGKTLTLDVPKTQSKDKVVPVPPTDKPSTTTPAALKQSDASKPP
                                                                                                                                                                                                                                                                                                                                             2678 TAAIQHQQKLGTPVTPKDSGDKPTDNASAPVGVSPVTPDGTPGAKPPPKDAPPVDDTK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              226 VKFSDPSKPNGQIWTGVIGSPAANAPDAGFPQRWFVVWLGTANNPVDKGAAKALAESIRP
                                           6 PNLTRRKGRLAALAIAAMASASLVTVAVPATANADPEPAPPVPTTAASPP-----STAAA
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ballinger D.G., Xue N., Harshman K.D.;
"A Drosophila photoreceptor cell-specific protein, calphotin, binds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a" to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  calcium and contains a leucine zipper.";
Proc. Natl Acad. Sci. U.S.A. 90:1536-1540(1993).
-! Natl Acad. Sci. U.S.A. 90:1536-1540(1993).
-! FUNCTION: Might function as a calcium-sequestering "sponge" regulate the amount of free cytoplasmic calcium. It binds 0. of Ca(2+) per mole of protein.
-! SUBUNIT: Homodimer (Probable).
-! SUBCELLULAR LOCATION: Cytoplasmic; hypodense compartment.
-! TISSUE SPECIFICITY: Soma and axons of photoreceptor cells of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             compound eyes and ocelli.
DEVELOPMENTAL STAGE: Expressed early in photoreceptor cell
122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera; Brachycera, Muscomorpha,
Bhydroidea, Drosophilidae, Drosophila.
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2824 AKSAAAPAAPAKSAAAPAAPAKSAAAPAAAPAKDQTKSA 2864
                                                                                                                                61 PPAPATPVAPPPPAAANTPNAQPGDPNAAPPPADPNAP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 286 L-VAPPPAPAPAPAPAPAPAPAGEVAPTPTTPTPORTLPA
152;
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01-OCT-1993 (Rel. 27, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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  Mismatches
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                                                                                                                                                                                                                                                                                                        ----HFDYGSALLSKTTGDPP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Canton-S;
MEDLINE=93165730; PubMed=8434015;
                                                                                                                                                                                                                   109 QPVRIDNPVGGF------
31;
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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96;
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CPN OR CAP.
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  Matches
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[1]
SEQUENCE FROM N.A.
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NCBI TaxID=4097;
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SIGNAL
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                                                                                                                                                                                                                                                                                                        SEQUENCE
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P13983;
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 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                         399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    458
                                                                                                                                                                                                                                                                                                                                                                              290 ATLTTÄPETPALAPVVÄESQVÄÄNTVVÄTP--PTPÄPEP-ETIÄPPVVAETPEVASVAVA 346
                                                                                                                                                                                                                                                                                                                                                                                                                                             GSALLSKTTGD-----PPFPGQPPP--VANDT------RIVLGRLDQKLYASAEAT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            501
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                                                                                                                                                                                                                                                                                                                                 ETTPPVVPPVAAESIPAPVVATTPV-----PATLAVTDPDVTASAVPELPPVIAPSPV
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                                                                                                                                                                                                                                                                                                                    LAALAIAAMASASLVTVAVPAT----ANADP--EPAPPVPTTAASPPSTAAAPP---
                                                                                                                                                                                                                                                                                              Indels 133; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sorghum bicolor (Sorghum) (Sorghum vulgare).
Eukaryota, Viridiplantee, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoldeae, Andropogoneae, Sorghum.
                                                                                                                                                                                                                                                                         Score 197.5; DB 1; Length 865; Pred. No. 0.002;
                                                                                                                                                                                                                                                                                                                                                            ----APATPVAPPPPA----AANTPNAQPGDPNAAPPPADPNAPP----
                                                                                                                       A -> AVABAVVA (IN REF. 2).
I -> T (IN REF. 2).
T -> A (IN REF. 2).
P -> A (IN REF. 2).
P -> PP (IN REF. 2).
I -> V (IN REF. 2).
A -> E (IN REF. 2).
B -> T (IN REF. 2).
C -> L (IN REF. 2).
D -> E (IN REF. 2).
W; 2110417E0B057CFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                     -----PPVIAPNAPQPVRIDNPVGGFSFALPAGWVESD----
                                                                                                                                                                                                                                                                    | | | : :: | | : :: | | EPPAPIPDLLEQTTSVPAVEAAESTSSPIPETSLP 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAPA--------PAGEVAPTPTTPQRTLP 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P24152;
01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Extensin precursor (Proline-rich glycoprotein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 283 A.A.
                                                                                            FlyBase, FBgn0010218; Cpn.
GO; GO:0005509; F:calcium ion binding; IDA
institutions as long
                                                                                                                                                                                                                                           721 E
84781 MW;
                                                   EMBL; LO2111; AAA28405.1; -. ERBL; LO5080; AAA28420.1; -. PIR; A47282; A47282.
PIR; A47283; A47282.
                                                                                                                                                                                                                                                                                                Conservative
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43
64
100
1127
1127
1158
1160
703
                                                                                                                                                                                                                                                     865 AA;
                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                  Calcium-binding
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CONFLICT
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CONFLICT
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                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                  CONFLICT
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EXTN SORET

D D 24152
DT 01-MAR
DT 30-MAR
DT 30-MAR
DT 30-MAR
DE Extens
GN HRGP.
OC EUKARY
OC SPETMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DANGVSGSASYYEVKFSDPSKPNGQIWTGVIGSPAANAPDAGPPQRWFVVWLGTANNPVD 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 ADPNAPPPPVIAPNAPQPVRIDNPVGGFSFALPAGWVESDAAHFDYGSALLSKTTGDPPF 152
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                                                                                                                                                           -!- FUNCTION: Structural component in primary cell wall.
-!- PTM: EXTENSINS CONTAIN A CHARACTERISTIC REPEAT OF THE PENTAPEPTIDE SER-PRO(4). THE PROLINE RESIDUE IS HYDROXYLATED AND THEN GLYCOSYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nicotiana tabacum (Common tobacco).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; asterids;
Lamiids; Solanales; Solanaceae; Nicotiana.
                                                              Raz R., Cretin C., Puigdomenech P., Martinez-Izquierdo J.A.; "The sequence of a hydroxyproline-rich glycoprotein gene from Sorghum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 PATANADPEPAPPVPTTAASPPSTAAAPPAPATPVAPPPPAAANTPNAQPG-DPNAAPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 PPTYTPSPKPTPP-PATPKPTPPTYTPSPKPKSPVYPPPPKASTPPTYTPSPKPPATKPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KGAA-----KALAESIRPLVAPP---PAPAPAPAPAPAPAPAGEVAPTTPTFP 319
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16-OCT-2001 (Rel. 40, Last annotation update)
Extensin precursor (Cell wall hydroxyproline-rich glycoprotein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003882; Pistil extensin.
PRINTS; PR01218; PSTLEXTENSĪN.
Repeat; Cell wall; Glycoprotein; Signal; Structural protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
EXTENSIN.
8D7FCD0DA8ED2D90 CRC64;
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                                                                                                                            vulgare.";
Plant Mol. Biol. 16:365-367(1991).
-!- FUNCTION: Structural component
TISSUE=Leaf;
MEDLINE=91370882; PubMed=1893107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 TYP-TPKPATKPPTP-PVYTPSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29593 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X56010; CAA39485.1; -. PIR; S13383; S13383.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PKPTPPV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 71; Conserv
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(Rel. 43, Last annotation update)

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L5-MAR-2004
                               channel 4.
                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 KLYASAEATDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFSDPS 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233 KPNGQIWTGVIGSPAANAPDAGPPQRWFVVWLGTANNPVDKGAAKALAESIRPLVAPPPA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              264 TYSPPPPAYAQSPQPSPTYSPPPPSPTYSPPPSPTYSPPPAYSPSPSPPTPTFSPPPA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75 AANTPNAQPGDPNAAPPPADP-NAPPPVIAP------NAPQPVRIDNPVGGFS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 TVAVPATANA-DPEP----APPVPTTAASPPSTAAAPPAAP-----TPV-APPPA 74
                                                                                                                  SUBCELLUTAR LOCATION: Extracellular matrix.
THE PRINTENSINS CONTAIN A CHARACTERISTIC REPEAT OF THE PENTAPEPTIDE SER-PRO(4). THE PROLINE RESIDUE IS HYDROXYLATED AND THEN GLYCOSYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                      EXTENSIN.
HA-P-P.
12 X 7 AA TANDEM REPEATS OF T-H-R-P-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------GQPPPVANDTRIVLGRLDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     384 -PPPPTYEQSPPPPPAYSPPLPAPPTYSPPPPTYSPPPPTYAQPPPL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----PPPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21; Mismatches 102; Indels 126; Gaps
                                                                          in
the
            Keller B., Lamb C.J., Respectfic expression of a novel cell wall hydroxyproline-rich slycoprotein gene in lateral root initiation.", Genes Dev. 3.1639-1646(1989).
-!- FUNCTION: Has a specialized structural function, possibly the mechanical penetration of the cortex and epidermis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.
CONTAINS THE SER-PRO(4) REPEATS.
                                                                                                                                                                                                                                                                                                             EMBL; X13885; CAA32090.1; -.
PIR, S06733; S06733.
InterPro; IPPR000480; Glutelin.
PRINTS; PR00211; GLUTELIN.
Repeat; Cell wall; Glycoprotein; Signal; Structural protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 X APPROXIMATE TANDEM REPEATS 641DD2278AB28524 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9JXĀ7; Q9QZW4;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 FALPAGWVESDAAHFDYGSALLSKTTGDPPFP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    479 YSPPPPSPIYSPPPP-OVOPLPPTESPPPRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293 PAPAPAEPAPAPAGEVAPTPTT---PTPQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----ppiyspppaysppppyaysppp----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 193;
                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
MEDLINE=90128263; PubMed=2612909;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.2%;
25.0%;
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70
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229
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236
205
620 AA;
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                                                                                                                                                                                                                                                                                                                                                                                           Hydroxylation.
                                                                                                       main root
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HCN4_RAT
ID HCN4_RAT
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Best Local
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REPEAT
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REPEAT
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To sour stimuli.";

In Nature 413:361-66362001)

Contraction and inactivation exhibiting weak selectivity for activation and inactivation exhibiting weak selectivity for potassium over sodium ions. May contribute to the native pacemaker currents in heart (If) and in neurons (Ih). Activated by CAMP. May mediate responses to sour stimuli.

Contracts in heart (If) and in neurons (Ih). Activated by CAMP. May mediate responses to sour stimuli.

Contracts in heart (If) and in neurons (Ih). Activated by CAMP. May mediate responses to sour stimuli.

Contracts complex of pore-forming subunits.

Contracts PRECIFICITY: Highly expressed in pyramidal and granule supraoptic nucleus in thatamus anterior nucleus, in the supraoptic nucleus in hypothalamus, in cerebellum, and in trapezoid nuclei and superior clulvary complex in the auditory system. Detected in a subset of elongated cells in teate buds.

Contracterized by a series of positively charged amino acids at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21530492; PubMed=11675786; Stevens D.R., Seidert R., Bufe B., Mueller F., Kremmer B., Gauss R., Stevens D.R., Kaupp U.B., Lindemann B.; "Hyperpolarization-activated channels HCN1 and HCN4 mediate responses
                                                                                                            Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                      STRAIN=Sprague-Dawley, TISSUE=Brain, MEDLINE=20457301; PubMed=11000485; Monteggia L.M., Eisch A.J., Tang M.D., Kaczmarek L.K., Nestler E.J.; "Cloning and localization of the hyperpolarization-activated cyclic nucleotide-gated channel family in rat brain."; Brain Res. Mol. Brain Res. 81:129-139(2000).
                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Heart,
MEDLINE=99459217; PubMed=10400919;
Shi W., Wymore R., Yu H., Wu J., Wymore R.T., Pan Z., Robinson R.B.,
Dixon J.E., McKinnon D., Cohen I.S.;
"Distribution and prevalence of hyperpolarization-activated cation
channel (HCN) mRNA expression in cardiac tissues.";
                        Potassium/sodium hyperpolarization-activated cyclic nucleotide-gated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF247453; AAF62176.1; -.
EMBL; AF155166; AAF01493.1; -.
InterPro; IPR00592; cmb_binding.
InterPro; IPR005821; Ion_trans.
InterPro; IPR005821; Ion_trans.
InterPro; IPR00520; M+channel_nlg.
Pfam; PF000520; cmM_binding; 1.
Pfam; PF000520; ion_trans; 1.
SMART; SM00100; cNMP; 1.
PR051TE; PS00889; CNMP_BINDING 1; 1.
PROSITE; PS00889; CNMP_BINDING 2; FALSE_NEG.
PROSITE; PS00842; CNMP_BINDING 3; 1.
Transport; Ion_transport; Ionic_channel; Voltage-gated channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 every third position. SIMILARITY: Belongs to the potassium channel family. HCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
                                                                                                                                                                                                   AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION, AND TISSUE SPECIFICITY.
                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 262-428 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Circ. Res. 85:1-6(1999).
                                                                                         Rattus norvegicus (Rat).
                                                                                                                                                                                                     SEQUENCE FROM N.A.,
                                                                                                                                                       NCBI_TaxID=10116;
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944 LPGARGGLGLLEHFLPPPPSSRSPSSSPGQLGQPPGELSPGLAAGPPSTPETPPRPERPS 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1054 PASSPPPPQVPQRRGTPPLTPGRLTQDLKLISASQPALPQDGAQTLRRASPHSSGBSMAA 1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----RAGGGSGSG----GLGPPGRPYGAIPGGHVTLPRKTSSGSLP 1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 --VIAPNAPOPVRIDNPVGGFSFALPAGWVESDAAHF------DYGSALLSKTTGDP 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 PFPGQPPPVANDTR----IVLGRLDQKL---YASAEATDSKAAARL-----GSDMGE 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      884 PGACSSPPAPTPSTSTAATTTGFGHFHKALGGSLSSSDSPLLTPLQPGARSPQAAQPPPP 943
Potassium channel; Potassium; Potassium transport; Sodium transport;
T CAMP; CAMP. Dinding; Transmembrane; Glycoprotein; Sodium channel.
T PRANSMEM 294 314 CT 267 CF CEGNENT SI (POTENTIAL).
T TRANSMEM 294 314 SEGMENT S2 (POTENTIAL).
T TRANSMEM 341 340 CTYOPLASNIC (POTENTIAL).
T TRANSMEM 341 340 CTYOPLASNIC (POTENTIAL).
T TRANSMEM 341 361 SEGMENT S3 (POTENTIAL).
T TRANSMEM 421 441 SEGMENT S6 (POTENTIAL).
T TRANSMEM 465 466 SEGMENT S6 (POTENTIAL).
T TRANSMEM 457 517 CYTOPLASNIC (POTENTIAL).
T DOMAIN 518 1198 CYTOPLASNIC (POTENTIAL).
T DOMAIN 518 1198 CYTOPLASNIC (POTENTIAL).
T DOMAIN 518 1198 CYTOPLASNIC (POTENTIAL).
T DOMAIN S18 1198 CYTOPLASNIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----TPVAP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
11.2%; Score 192.5; DB 1; Length 1198;
Best Local Similarity 23.8%; Pred. No. 0.0047;
Matches 98; Conservative 37; Mismatches 124; Indels 153; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----PLSLFGARASSGGPPLTAAPQREPGARSEPVRSKLPS 1196
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                                                                                                                                                                                                                                                                                                                       CAMP.
PRO/SER-RICH.
N-LINKED (GLCNAC. .) (POTENTIAL).
I -> V (IN REF. 2).
O MW; 6B92B8F9452F760F CRC64;
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799 107
458 45
404 40
1198 AA;
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Search completed: July 7, 2004, 18:21:51 Job time : 28.5 secs

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SE REPRESENTATION OF SERVICE S
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1726
1 MHQVDPNLTRRKGRLAALAI......PAGEVAPTPTTPTPQRTLPA 325
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                      OM protein - protein search, using sw model
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1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_nnan:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_nnc:*
7: sp_phage:*
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

|           | Description                   | O9r640 mycobacteri | O9f4h9 mycobacteri | OBVS65 mycobacteri | O65553 bovine hero | Ogask4 orvza sativ | O7t5d9 simian hern | O951d0 sus scrofa | 095id1 sus scrofa | 089x06 bradvrhizob | 07t591 simian herp | 08w5k6 orvza sativ | 07xh56 orvza sativ | 041805 zea mays (m | O8mxu8 caenorhabdi | O82du7 streptomyce | Q41645 volvox cart |
|-----------|-------------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| 071777700 | ΩI                            | O9R640             | O9F4H9             | 087865             | Q65553             | Q9ASK4             | Q7T5D9             | Q95JD0            | Q95JD1            | 90X68Q             | Q7T591             | OSWSK6             | Q7XH56             | 041805             | OBMXUB             | 082DU7             | Q41645             |
|           | DB                            | 7                  | 7                  | ~                  | 12                 | 10                 | 12                 | 9                 | 9                 | 16                 | 12                 | 10                 | 10                 | 10                 | ហ                  | 16                 | 10                 |
|           | °<br>Query<br>Match Length DB | 286                | 368                | 194                | 3247               | 698                | 3288               | 511               | 566               | 745                | 3326               | 1269               | 1269               | 1188               | 668                | 584                | 464                |
| ok        | Query<br>Match                | 89.2               | 61.0               | 32.9               | 14.8               | 14.4               | 14.4               | 14.1              | 14.1              | 14.0               | 13.9               | 13.8               | 13.8               | 13.8               | 13.4               | 13.4               | 13.2               |
|           | Score                         | 1539               | 1053.5             | 568                | 256                | 248.5              | 248                | 244               | 244               | 241.5              | 240.5              | 238                | 238                | 237.5              | 231                | 230.5              | 228.5              |
|           | Result<br>No.                 |                    | 73                 | m                  | 4                  | ហ                  | 9                  | 7                 | α                 | ov                 | 10                 | 11                 | 12                 | 13                 | 14                 | 15                 | 16                 |

| -22   | Q8vkn7 mycobacteri |      | O8fm53 corvnebacte | rosophila | 0941z6 arabidopsis | O95jc9 sus scrofa | eg       | 09lv48 arabidopsis | Ε   | н    | O9sbml volvox cart |       |     | 023635 caenorhabdi | O7u818 synechococc |          | ໝ      | Q948y7 volvox cart | O9spm0 zea mays (m | arrowia l | 084zl0 oryza sativ | arabid   | P89459 herbes simp | cantha       |          | O96q04 homo sapien | 3 gossypium | Q98f98 rhizobium l |
|-------|--------------------|------|--------------------|-----------|--------------------|-------------------|----------|--------------------|-----|------|--------------------|-------|-----|--------------------|--------------------|----------|--------|--------------------|--------------------|-----------|--------------------|----------|--------------------|--------------|----------|--------------------|-------------|--------------------|
| α     | 6 Q8VKN7           |      | 6 Q8FM53           |           | 0                  |                   | 2 039266 | 0                  |     |      | 0 Q9SBM1           |       |     | 023635             | 6 Q7U8L8           | 0 Q9XIB6 | 007229 | O                  | C                  |           | 0                  | 0 Q9TOK5 |                    | 093107       | 5 O9F2N5 | 96004              |             | 6 Q98F98           |
| 652 4 | 98                 | 22 1 | 60                 | 20        | 652 1              | 26                | 34 1     | 652 1              | m   | 84 1 | 09 1               | 39 1  | Н   |                    |                    | 847 1    | •      | Н                  | Н                  |           | Н                  | **       | 7                  | <u> </u>     | m.       | 1480 4             | 1           | 10                 |
| 13.2  | ٠                  | ω.   | ٠                  | 13.1      | ë.                 | •                 | 'n       | 12.9               | ς.  | 12.9 | ά.                 | •     | ς.  | 9.                 | 5.                 | 'n.      | r.     | 4.                 | 4.                 | 4.        | 4.                 | 4.       | 4.                 | ۳.           | ۲.       | ۲.                 | ٠.          | 0.                 |
| 227.5 | 22                 | 'n   | 'n                 | 225.5     | 'n                 | 225               | 224.5    | 23.                | 222 | 222  | 218                | 217.5 | 217 | 217                | 16.                | 216.5    | 15.    | 14                 | 214.5              | 214       | 214                | 213.5    | 'n.                | $\leftarrow$ | Н        | $\circ$            | 208.5       |                    |
| 17    | 18                 | 19   | 20                 | 21        | 22                 | 23                | 24       | 25                 | 56  | 27   | 28                 | 29    | 30  | 31                 | 32                 | 33       | 34     | 32                 | 36                 | 37        | 38                 | 6 E      | 40                 | 41           | 42       | 43                 | 44          | 45                 |

### ALIGNMENTS

|                  |                           |                             |                 |                     |                     |                    |                                                              |                                                     |             |     |           |                                   |                                                         |                                       |                       |                           |                                           |                                                                            | ó                                              | 0.                                                              | 0                                                               | 159             | 120                                                            | 219                                                             | 180                                                             | 279                                                             |
|------------------|---------------------------|-----------------------------|-----------------|---------------------|---------------------|--------------------|--------------------------------------------------------------|-----------------------------------------------------|-------------|-----|-----------|-----------------------------------|---------------------------------------------------------|---------------------------------------|-----------------------|---------------------------|-------------------------------------------|----------------------------------------------------------------------------|------------------------------------------------|-----------------------------------------------------------------|-----------------------------------------------------------------|-----------------|----------------------------------------------------------------|-----------------------------------------------------------------|-----------------------------------------------------------------|-----------------------------------------------------------------|
|                  | PRELIMINARY; PRT; 286 AA. | 00 (TrEMBLrel. 13, Created) | (TrEMBLrel, 13, | PrEMBLrel. 25, Last | CULTURE FILTRATE gl | rium tuberculosis. | Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; | Corynebacterineae; Mycobacteriaceae; Mycobacterium. | TaxID=1773; |     |           | MEDLINE=96196153; PubMed=8626314; | ., Khoo K.H., Swiderek K.M. Brennan P.J., Belisle J.T., | of the full extent of glycosylation o | of Mycobacterium tube | iol. 178:2498-2506(1996). | 286 AA; 28764 MW; 4BETAD89FEB42493 CRC64; | 89.2%; Score 1539; DB 2; Length 286;<br>nilarity 99.7%; Pred. No. 1.3e-89; | ; Conservative 1; Mismatches 0; Indels 0; Gaps | DPEFAAPPVFITAASPPSTAAAPPAPATPVAPPPPAAANTPNAQPGDFNAAPPPADPNAPP 9 | DPEPAPPVETTAASPPSTAAAPPAPATFVAPPPPAAANTPNAQPGDPNAAPPPADFNAPP 60 | KTTGDPPFPGQPPPV | PPVIAPNAPQPVRIDNPVGGFSFALPAGWVESDAAHFDYGSALLAKTTGDPPFFGQPPPV 1 | ANDTRIVLGRLDQKLYASABATDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSG 21 | ANDTRIVLGREDOKLYASABATDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSG 18 | SASYYEVKFSDFSKPNGQIWIGYIGSFAANAPDAGPPORWFVVWLGTANNPVDKGAAKAL 27 |
| LT 1             | Q9R640                    | 01-MAY-2000                 | 01-MAY-2000     | 01-OCT-2003         | MPT-32=45 kDa       | Mycobacterium      | Bacteria;                                                    | Corynebac                                           | NCBI Taxi   | [1] | SEQUENCE. | MEDLINE=9                         | Dobos K.M.,                                             | "Definiti                             | glycoprotein          | J. Bacteriol.             | SEQUENCE                                  | atch<br>cal                                                                | Marches 285;                                   | 40                                                              | 1                                                               | 100             | 19                                                             | 160                                                             | 121                                                             | 220                                                             |
| RESULT<br>09R640 | OH Z                      | D T                         | DŢ              | H                   | DE                  | SO                 | ပ္ပ                                                          | ႘                                                   | XO          | RN  | КP        | RX                                | RA                                                      | RT                                    | R                     | RL                        | Š                                         | S B S                                                                      | Σ<br>E                                         | ઠે                                                              | Ωþ                                                              | ò               | С                                                              | ò                                                               | QQ                                                              | ò                                                               |

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 PPAPATPVAPPPPAA----ANTPNAQ------PGDPNAAPPP--ADPNAPPPVIAPN 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55 PPAAPAPNGQPAPNAQPAPGAPAPNGQPAPAAPAPAPDPNGAPPVGAPPNGAPPPVDPN 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1] SEQUENCE FROM N.A.
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SECOLT T.B., Lin T.L., Wu C.C.;
"Characterization of fibronectin binding by Mycobacterium avium subsp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67; Gaps
                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Fibronectin-attachment protein FAP-P (Fibronectin-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dheenadhayalan V., Chang Y.F.; "Mycobacterium avium subsp. paratuberculosis fibronectin-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.0%; Score 1053.5; DB 2; Length 368; 60.0%; Pred. No. 6.8e-59; vative 24; Mismatches 61; Indels 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium paratuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1770;
                                                                       AESIRPLVAPPPAPAPAPABPAPAPAPAGEVAPTPTTPTPQRTLPA 325
                                                                                                         Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY007557; AAG2211.1; -
EMBL; AF334165, AAK20194.1; -
SEQUENCE 368 Aa, 36116 MW; 4B22A27730C54337 CRC64;
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RESULT 3 Q8VS65

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162 DIRIVIGRIDOKLYASABATDSKAAARLGSDMGBFYMPYPGTRINQETVSLD-ANGVSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           221 ASYYEVKFSDPSKPNGQIWTGYIGSPAANAPDAGPPQRWFVVWLGTANNPVDKGAAKALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ASYYEVKFSDASKPNGQIWTGVIGS-----ANGGNAQRWFVVWLGTSNDPVDKVAAKALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     281 ESIR---PLVAPPPAP-----APAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G., Misra
                                                                                                                                                                                                                                                                                                                                                                                      40;
                                                                                               Mycobacterium paratuberculosis,
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1770;
                                                                                                                                                                                                                                                                                                                                                          Length 194;
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 63.9%; Pred. No. 1.3e-28;
Matches 124; Conservative 14; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schwyzer M., Styger D., Vogt B., Lowery D.E., Simard C., LaBoissiere S., Misra V., Vlcek C., Paces V.; Vet. Microbiol. 0:0-0(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=COOPER,
Schwyzer M., Vloek C., Lowery D.E., Bello L.J., Meyer G.
Thiry E., Pacces V.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                            194 AA; 19339 MW; 3AEB7CBC893DF292 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovine herpesvirus 1.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
NCBI_TaxID=10320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
                       01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Fibronectin-attachment mutant protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176 VEVSPTP-TPTPQQ 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   308 GEVAPTPTTPOR 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-179 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. (TrEMBLrel. (TrEMBLrel. 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
PRELIMINARY;
                                                                                                                                                                           SEQUENCE FROM N.A.
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280 115 307

us-10-720-192-2.rspt

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122 SPVQQPPVA-----ASPPPSSPADLPPPNPPAR--SDTPPVVQSPPPHRKSPRTP 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      211 SIDANGVSGSASYYEVKFSDPSKPNGQİWTGVIGSPAANAPDAGPPORWFVVWLGTANNP 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171 WAPPMAPSPSGS-----PTKP----SPASPSPIAGDP-----IIPTPNNP 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 AVPATANADPEPAPPVPTTAASPPSTAAAPPAAPPATPVAPPPAAANTPNAQPGDPNAAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PADPNAPPPPVIAPNAPQPVRIDNPVGGFSFALPAGWVESDAAHFDYGSALLSKTTGDPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 PAPPVAVPPPATVPPPPVPVASPPPT-----PSATLPPPSPPASVPVPPTPATTPPKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152 FPGQPPPVANDTRIVLGRLDQKLYASAEATDSKAAARLGSDMGEFYM-PYPGTRINQETV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 ATPATAAAAPSTATPTP---ATQPNATPADPSTTPPAASPPLPSAATPPPQPDSPPSPP
                                                                                                                                                               EMBL; APU02862; DILLOLLER,

R Gramene; Q9ASK4; T.

R GO; GO:0005524; F:AT-

DR GO; GO:0005524; F:Protein serine/threonine kinase activity; IEA.

GO; GO:0006740; F:transferase activity; IEA.

DR GO; GO:0006740; F:transferase activity; IEA.

DR GO; GO:0006740; F:transferase activity; IEA.

DR GO; GO:0006740; F:COTE kinase activity; IEA.

DR InterPro; IPR008271; Ser_thr_pkin_AS.

DR Probom; PR00089; Pintase; I.

DR PROSITE; PS001001; PROTEIN KINASE ATP; 1.

DR PROSITE; PS001001; PROTEIN KINASE ATP; 1.

DR PROSITE; PS00100; PROTEIN KINASE ST; 1.

KW HYPOCHACICAL protein; ATP-binding; Kinase;

Serine/threonine-protein kinase; Transferase.

RROJENCE 698 AA; 72733 MW; F3886E46DCA9DAE6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete Sequence and Comparative Analysis of the Genome of Herpes Virus (Cercopithecine Herpesvirus 1) from a Rhesus Monkey.";
J. Virol. 77:6167-6177(2003).
                                                                                                                   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
EMBL; AP002882; BAB39873.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 271 VDKGAAKALAESIRPLVAPPPAAPAPAEPAPAPAPAGEVAPTPTTPQ 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSPLATPSAPGSGTPVVT-PSAPVSGPPSPGTAPATAADRSNKSLSPNTQ 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-22628476; PubMed-12743273;
Perelygina L., Zhu L., Zurkuhlen H., Mills R., Borodovsky M.,
Hilliard J.K.;
                        STRAIN=cv. Nipponbare;
Sasski, T., Mateumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
clone:P0439B06.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79C391EE8E6F7983 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Simian herpes B virus (Cercopithecid herpesvirus 1)
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-007-2003 (TrEMBLrel. 25, Created)
01-00T-2003 (TrEMBLrel. 25, Last sequence update)
01-00T-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 14.4%; Score 248.5; DB 10; Local Similarity 30.7%; Pred. No. 7.5e-08; les 89; Conservative 20; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF533768; AAP41454.1; -. SEQUENCE 3288 AA; 342496 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Very large tegument protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2644 PAPPLPPAPLPPAPLPPAPSTAPVPAPPLPPPALTPALTPALTPAPTPAPLPLP 2703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |: : :|| | : :|
2704 API---TVLVPAP-VPAFAP-----IPAPAPTPAPAPTPAPPTPPAPDAPDGAMGALSATRR 2754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2807 -PSRPPSL-----EPVPGLP--LPPSR------VQAPVDAPAPPPAPERPAPPAP 2848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PATPVAPP-PPAAANTPNAQPGDPNAAPPPADPNAP-----PPPVIAPNAPQPVRID 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 LYASAERATDSKAAA----RLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFS 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 NPVGGFSFALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQP-PPVANDTRIVLGRLDQK 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DPSKPNGQIWTGVIGSPAANAPDAGPPQRWFVVWLGTANNPVDKGAAKALAESIRPLVAP 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LTR----RKGRLAALAIAAMASASLVTVAVPATANADPEPAPPVPTTAASPPSTAAAPPA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2755 PTRRAGARKSLPAAQPRQRLLRSRSPASVPAPGS----ELVPPPSGGALGSPPSFV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                            Meyer G., Misra V.;
                                                                                                                                  Schwyzer M., Styger D., Vogt B., Lowery D.E., Simard C., LaBoissiere S., Misra V., Vlcek C., Paces V.; "Gene contents in a 31-kb segment at the left genome end of bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa (Rice).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta, Liliopsida, Poales, Poaceae,
Enhartoideae, Oryzeae, Oryza.
NCBL_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 12; Length 3247;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Schwyzer M.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; 278205; CABO16051;
EMBL; 27004801; CAA06097.1;
InterPro; IPR006210; Herpes teg N.
InterPro; IPR006210; Herpes teg N.
Pfam; PF04843; Herpes teg N.
Pfam; PF04866; Herpes UL36; 1.
SEQUENCE 3247 AA; 332190 MW; 3AEAA72F8F001F6A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.8%; Score 256; DB 12; Length 3 31.2%; Pred. No. 1.4e-07; .ive 20; Mismatches 153; Indels
                   bmitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                   STRAIN=JURA;
Schwyzer M., Vlcek C., Lowery D.E., Bello L.J., Meyer G.
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2849 ERPAPPAPERPAPPAPERPAPP----PAPERPAP 2880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   290 P-PAPAPAPAPAPAPAGEVAPTPTTPQRTLP 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     698 AA.
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                                                                                                           MEDLINE=97164286; PubMed=9010999;
                                                                                                                                                                                                                               Vet. Microbiol. 53:67-77(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ol-JUN-2001 (TrEMBLrel. 17, C. 01-JUN-2001 (TrEMBLrel. 17, Le 01-OCT-2003 (TrEMBLrel. 25, La Hypothetical protein. P0439B06.8.
                                                               SEQUENCE OF 1-179 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                         herpesvirus-1.
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Schwyzer
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Matches

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RAPRET REPRESENTATION OF SECOND OF S

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Indels

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125 PPPPGPPPPGARPPPGARPPPGPP-----PAGGLQQGPAPSHVG----PKKKPPPPG 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---PPSPPANDSQEG--SPPSADGPQQGPAP-----SGDK 225
152 --FPGQPPPVANDTRIVLGRLDQKLYASAEATDSKAAARLGSDMGBFYMPYPGTRINQET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 PATANADPEPAPVPITAASPPSTAAAPPAPATPVAPPPPAAANTPNAQPGDPNAAPPPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94 -DPNAPPPPVIAPNAPQPVRIDNPVGGFSFALPAGWVESDAAHFDYGSALLSKTTGDPP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tieche J.-M., Leonora J.; "Cloning and expression of a novel proline-rich protein from porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE=Parotid gland;
Zhang Q., Szalay A.A., Kyeyune-Nyombi E., Sands J.F., Oberg K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 270 PVDXGAAKALAESIRPLVAPPPAPAPAPAPAPAPAPAGEVAPTPTTPTP 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 100;
                                                                                                                          270 PVDKGAAKALAESIRPLVAPPPAPAPAPAEPAPAPAPAGEVAPTFTTPTP 319
                                                                                                                                                                                                      265
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyzhizobiaceae; Bradyrhizobium.
NCBL_TaxID=375;
                                                                                                                                                                                             226 pkkkpp------ppagpppppppppppppppg------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   parotid glands.";

Submitted (MAY-201) to the EMBL/GenBank/DDBJ databases.

EMBL, AY035847, AAK61381.1;

GO, GO:0005199; F:structural constituent of cell wall; IEA.

HIGGEROPS, IPROJABLES, PISCHI, extensin.

PRINTS, FROLISH PSTLEXIENSIN.

SEQUENCE 566 AA, 53213 MW; E33B3B5E1BDEBB1A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
NCBI TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 095JD1,
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DCT-2003 (TrEMBLrel. 25, Last annotation update)
Basic proline-rich protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           745 AA
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01-JUN-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2003 (TrEMBLrel. 01-OCT-2003 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DAGPPORWEVVWLGTANNPVDXGAAKALAESIRPLVAPP----PAPAPAPAEPAPAPA 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDPPFPGQP-----PPVANDTRIVLG-----RLDQKLYASAEATDSKAAAR-----LGS 191
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                                                                                                                                                                                                                      TVAVPATANADPEPAPPVPTTAASPPSTAAAPPAPPATPVAPPPPAAANTPNAQPGDPNAA
                                                                                                                                                                                                                                                                                                      90 PPPADPNAPPPPV--IAPNAPQPVRIDNPVGGFSFALPAGWVESDAAHFDYGSALLSKTT
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TISSUE-Parotid gland;
Zhang Q., Szalay A.A., Kyeyune-Nyombi E., Sands J.F., Oberg K.C.,
Tieche J.-M., Leonora J.;
"Cloning and expression of a novel proline-rich protein from porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Sus.
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10, Mismatches 99; Indels 100;
                                                                                                                                               40;
                                                          Length 3288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.1%; Score 244; DB 6; Length 511; 27.9%; Pred. No. 1e-07;
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY035848; AAK61382.1; -.
GO, GO:0005199; F:Structural constituent of cell wall; IEA.
InterPro; IPR003882; Pistil extensin.
PRINTS; PR01218; PSTLEXTENSIN.
                                                                                                                                               Indels
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
NCBI_TaxID=9823;
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Last annotation update)
                                                               ; Score 248; DB 12;
; Pred. No. 4.4e-07;
24; Mismatches 150;
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                                                                           14.4%;
29.8%;
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1; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   206 NQETVSLDANGVSGSASYYEVKFSDPSKPNGQIWTGVIGSPAANAPDAGPPQRWFVVWLG 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47 VPTTAASPPSTAAAPP---APATPVAPPPPAAANTPNAQPGDPNAAPPPAADPNAP-PPPV 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 АРРРАДДРУНРРАДРУРДДДРУРДРДРУРРР--РРАДКРДРУРРРРРУДДРКОРЅРРРА 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IAP--NAPQPVRIDNPVGGFSFALPAGWVESDAAHFDYGSALLSKTTGDP-PFPGQPPPV 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 AAPQQHAPTP---PPPAPPAARPAPTPPAPPPAAAPQHAPPPPPPAARPTPTPPPPA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T---ANNPVDKGAAKALAESIRP--LVAPP-----PA--PAPAPAEPAP--APAPAGEVA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 GPAARPT-----PAPTATPTPVAPPPAAPTARPGS------PAPAATPAPTPA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPPAAGSPPAPGATPAPTTTPAPGGTATPPSGRPGPASTPAPGAATPAPTAPAPGGALT 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LATTALTAMOLANTASHAQGASPLVVAQAQPQETGPDGKPKQPPKGPPGAAPPAAPARPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 ANDTRIVLGRIDOKLYASABATDSKAA-----ARLGSDMGBFYMPYPG-----TRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   228 PTATPAPTATPAPGSTP-----VRPG
                                                                                   Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.,
                                                                                                                                                                                        "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002)
EMBL; AP005936; BAC45786.1; -.
EMBL; AP005524; F.ATP binding; IEA.
GO; GO:0004672; F.protein Kinase activity; IEA.
GO; GO:0004672; F.protein Rinase activity; IEA.
GO; GO:000584; F:sprotein amino acid phosphorylation; IEA.
InterPro; IPR003882; Pistil extensin.
InterPro; IPR00319; Prot_Kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 LAALAIAAM-----ASASLVTVAVPATANADPEP------APP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 16; Length 745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Shbv)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.0%; Score 241.5; DB 16; Length 29.6%; Pred. No. 2.2e-07; ive 16; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        745 AA; 74545 MW; 155EDFCC74DBCF6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Simian herpes B virus (Cercopithecid herpesvirus 1)
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
NCBI_TaxID=10325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
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                                                     MEDLINE=22484998; PubMed=12597275;
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MEDLINE=22607624; PubMed=12721804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR01218; PSTLEXTENSIN.
ProDom; PD000001; Prot_kinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPPGRPGAGPTPGPQGGTP 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTP-----TTPTPQRTLP 324
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(TrEMBLrel. 25, I
(TrEMBLrel. 25, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 112; Conservative
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UL36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00691; OmpA; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome.
SEQUENCE 745 AA;
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01-OCT-2003 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              323
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COTTS91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3114 R-----PPSPAAPDAGP-----AAASGPSGGVPAPRLGALVPGRVAVPRRQIPP 3157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2995 APAATPASPVPTPTSSLPTPPSKPPAFFQPSLATGGSVAPGGDFRRRAPSRPTAAVPAAP 3054
                                                                                                                                                                                                                                                                                                                                                       75 AANTENAQPGDENAAPPPADPNAPPPV--IAPNAPQPVRIDNPVGGFSFALPAGWVESD 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     237 QIWTGVIGSPAANAPDAGPPQRWFVVWLGTANNPVDKGAAKALAESIRPLVAPP----PA 292
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Wing R.A., Yu Y., Yang T.J., Nah G., Soderlund C., Chen M., Kim H.-R., Rambo T., Saski C., Henry D., Oates R., Simmons J.;
Rice Genomic Sequence.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AC079179; AAL31655.1;
EMBL; AC116601; AAM08709.1;
                                                                                                                                                                                                                                                                                                           17 ALAIAAMASASLVTVAVPATANADPEPAPPVPTTAASPPSTAAAPPAPATPVAP--PPPA
                                                                                                                                                                                                                                                                                                                                                                                                                                        133 AAHFDYGSALLSKTTGDPPFPGQP-----PPVANDTRIVLG-----RLDQKLYASAEATD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183 SKAAAR-----LGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFSDPSKPNG
                                                                                                                                                                                                                        Gaps
Obsawa K., Black D.H., Sato H., Rogers K., Eberle R.;
"Sequence and genetic arrangement of the UL region of the monkey B
virus (Cercopithecine herpesvirus 1) genome and comparison with the
region of other primate herpesviruses.";
Arch. Virol. 148:389-997(2003).
EBMBL, ABA056160; BACS8076.2; -.
SEQUENCE 3326 AA; 345566 MW; 6B53E3860F43CDF0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                            Length 3326;
                                                                                                                                                                                                                        41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. Wind R.A., Yu Y., Soderlund C., Chen M., Kim H.-R., Rambo Wing R.A., Yu Y., Cotes R., Simmons J.; Saski C., Henry D., Oates R., Simmons J.; Rambo Sequence "." Rice Genomic Sequence"; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
OSJNDAROUT9805.10 OR OSJNAA0079805.2.
Oryza sativa (Rice).
                                                                                                                                                                            DB 12;
                                                                                                                                                                          13.9%; Score 240.5; DB 12; 29.1%; Pred. No. 1.3e-06; Live 24; Mismatches 162;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        293 PAPAPAEPAPAPAGEVAP 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO, GO:0003779; F:actin binding;
InterPro; IPR008973; C2 CalB.
InterPro; IPR003104; FHZ.
                                                                                                                                                                                                 Local Similarity 29.1
Les 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF02181; FH2; 1.
SMART; SM00498; FH2; 1.
Hypothetical protein.
SEQUENCE 1269 AA; 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gramene; Q8W5K6;
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683 ÞEKSLPPP----TLIPSPPPQEK--PTPPSTPSKPPS------SPEKP 718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    769 PP-----APLSSPPAPAQVKSSPPPAPKSSPPLAPVSSPPQVEKTS 817
      ETVSLDANGVSGSASYYEVKFSDPSKPNGQIWTGVIGSPAANAPDAGPPQRWFVVWLGTA 267
                                                                                                                                                                                                        NNPVDKGAAKALAESIRPLVAPPPAPAPA----PAEPAPAPAGEVAPTPTTPORTL 323
                                                                                                                                                                                                                                                             NGP-----SAPAPPL--PPPLPAANKRNPPAPPPPLMTGKKAPAPPPPQAPK 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92 PADPNA-PPPPVIAPNAPQPVRIDNPVGGFSFALPAGWVESDAAHFDYGSALLSKTIGDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLDANGVSGSASYYEVKFSDPSKPNGQIWTGVIGSPAANAPDAGPPORWFVVWLGTANNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    569 PAPVASPPPVKSPPPPTLVÁSPPPPVKSPPPPÁ-PVÁSPPPVKSPP---PPTPVÁSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   625 PPAPVASSPPPMKSP--PPPTPVSSPPPPEKSPPPPPAKSTPPPEEYPTPPTSVKSSPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 PATANADPEP--APPVPTTAASPPSTAAAPPAAAPPVAPPPPAAANTPNAQPGDPNAAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN-373; TISSUD-Pollen; Rubinstein A.L., Broadwater A.H., Lowrey K., Bedinger P.A.; Rubinstein A.L., Broadwater A.H., Lowrey K., Bedinger P.A.; Rubinstein A.L., Droadwater A.H., Lowrey K., Bedinger P.A.; Rubinstein A.L., Droadwater A.H., Lowrey K., Bedinger P.A.; Submitted (UIN-1994) to the BMBL/GenBank/DDBJ databases. EMBL; Z34465; CAA84230.1; -. EMBL/GenBank/DDBJ databases. EMBL; S49915; S49915. InterPro; IPRO01611; LRR. InterPro; IPRO01611; LRR. InterPro; IRRO070909, LRR_Dlant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 POTENTIAL.
120981 MW; 2C77C7F8D7130149 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1993 (TrEMBLrel. 25, Last annotation update)
Extensin-like protein precursor.
Zea mays (Maize)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 237.5; DB 10;
; Pred. No. 6.6e-07;
30; Mismatches 123; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1188 AA
                                                                                                                                              RIPTGAATSSKGPPPPPPPPPPPANRTNGP-
13.8%;
28.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 1188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 87; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                              324 P 324
                                                                                                                                                                                                                                                                                                                                                                                  P 774
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
0SJNBA0079B05.10.
0SJNBA0079B05.10.
Crza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryzea.
                                                                                               78;
                                        Length 1269;
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The Rice Chromosome 10 Sequencing Consortium;
"In-depth view of structure, activity, and evolution of rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1269;
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Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
BMBL; AE017051; AAPS1898.1; -.
Hypothetical protein.
SEQUENCE 1269 AA; 138431 MW; 262E546481B25CA6 CRC64;
                                     13.8%; Score 238; DB 10; Length 1 27.2%; Pred. No. 6.6e-07; ive 20; Mismatches 121; Indels
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Pred. No. 6.6e-07;
0; Mismatches 121; Indels
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Best Local Similarity 27.2%; Pro
Matches 82; Conservative 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    397 DCGSAAPAATDSGYRSKRNAYGDEQVTPAPAAAAEAPADAPVEQAPVAVPAPAPAAAA--- 453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 AAAPAADAPVEQAPVAVPAPAPAAPAPDCGSAAPAAPAAPAATDSGYRSKRNSYGDE
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                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 13.4%; Score 231; DB 5; Length 668; Best Local Similarity 26.4%; Pred. No. 9e-07; Matches 107; Conservative 23; Mismatches 137; Indels 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Waterston R.; "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Waterston R.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, ACO06672, AAM98004.1;
WormPep; KOBD12.6; CE21047.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The sequence of C. elegans cosmid K08D12.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
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668 AA; 62778 MW; FB9ACC5739DC398A CRC64;
                                                              01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
10-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein K08D12.6.
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STRAIN-Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                 PRELIMINARY;
                                                                                                                                                                                                                             Caenorhabditis elegans.
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"Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis.";
Nat. Biotechnol. 21:226-531(2003).
EMBL; AP005040; BAC72583.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=MA.4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=2147403; PubMed=11572948;
MEDLINE=21477403; PubMed=11572948;
CMUTA S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T. Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary metabolites.";
                                                                                                                                                                             Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
VCBI_TaxID=33903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
13.4%; Score 230.5; DB 16; Length
Best Local Similarity 29.6%; Pred. No. 8.4e-07;
Matches 94; Conservative 16; Mismatches 113; Indels
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STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=22608306; PubMed=12692562;
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SEQUENCE 584 AA; 59261 MW; 7AA08D5F87EE2378 CRC64;
Created)
Last sequence update)
Last annotation update)
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24,
                                                                                                                                                                Streptomyces avermitilis.
(TrEMBLrel. 2 (TrEMBLrel. 2 (TrEMBLrel. 2
                                                                                     Hypothetical protein.
SAV4871.
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Job time : 39.5 secs
01-JUN-2003
01-JUN-2003
01-JUN-2003
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1 MHQVDPNLTRRKGRLAALAIAAMASASLVTVAVPATANADPEPAPPVPTTAASPPSTAAA
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amino acid
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Best Local Similarity 100.
Matches 325; Conservative
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US-08-382-184-2
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1016.875 Million cell updates/sec
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1726
1 MHQVDPNLTRRKGRLAALAI.......PAGEVAPTPTTPTPORTLPA 325
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Sequence 2, B
Sequence 6, B
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Sequence 3, B
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Sequence 2,
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                                                                 July 7, 2004, 18:21:10 ; Search time 16.5 Seconds
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  /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
  /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-132-528-3
US-09-599-366-2
US-09-599-366-3
US-09-985-372-3
US-09-985-372-3
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US-09-985-38-4
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Maximum Match 100%
Listing first 45 summaries
                                            protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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         Copyright
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Match ]
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Perfect score:
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US-U8-382-184-2

Sequence 2, Application US/08382184

Sequence 2, Application US/08382184

Sequence 2, Application US/08382184

Patent No. 5714593

TITLE OF INVENTION: MICROBACTERIAL PROTEINS,

TITLE OF INVENTION: MICROBACTERIAL PROTEINS,

TITLE OF INVENTION: AND FOR THE DEFECTION OF TUBERCULOSIS

NUMBER OF SEQUENCES: 3

ADDRESSEE: DELOY, SPITAK, MCLELLAND, MAIER &

ADDRESSEE: OBLOW, SPITAK, MCLELLAND, MAIER &

ADDRESSEE: NEUSTAAT, P.C.

STREET: 1755 S. Jefferson Davis Highway, Suite 400

STATE: Virginia

CONNERS, US.A.

ZIP: Z2202

CONPUTER: TABABLE FORM:

COMPUTER: THE PC-DOS/MS-DOS

SOFTWARE: PATENTION DATA:

COMPUTER: THE PC-DOS/MS-DOS

SOFTWARE: PATENTION DATA:

ATTORNEY/AGENT INFORMATION:

REFERENCE/DOCKET NUMBER: 22640720

TELESPHONE: 703-413-3200

TELESPHONE: 703-413-3200

TELESPHONE: 703-413-3200

TELESPHONE: 703-413-3200
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
2266666666666444444
80012666666666444444
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Gaps

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Length 325;

Score 1726; DB 1; Length Pred. No. 6.4e-127; Mismatches 0; Indels

0; Mismatches

240

120

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RESULT 3
US-09-132-528-2
US-09-132-528-2
Sequence 2, Application US/09132528A
Fatent No. 6221353
Fatent No. 6221353
GENERAL INFORMATION:
APPLICANT: LAQUEXRERIE, Anne
APPLICANT: RESCHER, Pascale
APPLICANT: RESCHER, Pascale
APPLICANT: ROMAIN. Pelix
TITLE OF INVENTION: AND THEIR USE FOR VACCINES AND FOR THE DETECTION OF
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 0660-0138-001V
CURRENT FILING DATE: 1996-04-30
CURRENT FILING DATE: 1996-04-30
NUMBER OF SEQ ID NOS: 5
SEQ ID NOS: 5
SEQ ID NOS: 5
SEQ ID NOS: 5
SEQ ID NOS: 2.1
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          PPAPATPVAPPPPAAANTPNAQPGDPNAAPPPADPNAPPPPVIAPNAPQPVRIDNPVGGF
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100.0%; Pred. No. 6.4e-127;
Live 0; Mismatches 0;
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US-09-132-528-2
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Best Local Similarity 100.
Matches 325; Conservative
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MICROOGGANISMS PRODUCING THEM AND THEIR USE FOR VACCINES
AND FOR THE DETECTION OF TUBERCULOSIS
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120
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PPAPATPVAPPPPAAANTPNAQPGDPNAAPPPADPNAPPPPVIAPNAPQPVRIDNPVGGF
                     SFALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPPVANDTRIVLGRLDQKLYASAEA
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COMPUTER: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/641,356
FILING DATE: 0.836
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/382,184
FILING DATE: 0.1-FEB-195
ATTORNEY AGENT INPORMATION:
NAME: OBLOW, NORMAN F
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 22,618
TELESCOMMUNICATION INFORMATION:
TELESCOMMUNICATION INFORMATION:
TELESCOMMUNICATION INFORMATION:
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100.0%; Pred. No. 6.4e-127;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                               APAPAPAGEVAPTPTTPTPQRTLPA 325
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Best Local Similarity 100.
Matches 325; Conservative
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TELEFAX: 703-413-2220
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MOLECULE TYPE: protein
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Virginia
: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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EARLIER FILING DATE: 1996-02-01
EARLIER APPLICATION NUMBER: 382184
FARLIER FILING DATE: 1995-02-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PAUGHTIN Ver. 2.0
IENGTH: 325
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US-09-599-366-2
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                                                                                                      Sequence 3, Application US/09132528A

Facent No. 6221353

GRUERAL INFORMATION:
APPLICANT: HADUEXPERIE, Anne
APPLICANT: PESCHER, Pascale
PPLICANT: PESCHER, PASCAL
APPLICANT: PESCHER, PASCAL
APPLICANT: POWAIN; Felix
ITILE OF INVENTION: MYCOBACTERIAL PROTEINS, MICORORGANISMS PRODUCING THEM
ITILE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 0660-0139-0D1V
CURRENT APPLICATION NUMBER: US/09/132, 528A
CURRENT FILING DATE: 1996-04-10

EARLIER PILING DATE: 1996-04-10

NUMBER OF SEQ ID NOS: 5
SOFUND NO 3
SEQ ID NO 3
SEG ID NO 3
SEG ID NO 3
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US-08-875-494-2

i Sequence 2, Application US/08875494

i Patent No. 6221610

i GENERAL INFORMATION:

i APPLICANT: LAQUERRELE, ANNE

APPLICANT: ROMAIN, FELIX

i TITLE OF INVENTION: MYCOBACTERIAL PROTEINS, MICROORGANISMS PRODUCING THEM

ITILE OF INVENTION: TUBERCULOSIS

ITILE OF INVENTION: TUBERCULOSIS

ITILE OF INVENTION: TUBERCULOSIS

ITILE OF INVENTION: UNBERGINGS

CURRENT APPLICATION NUMBER: US/08/875,494

CURRENT FILING DATE: 1997-08-01

EARLIER APPLICATION NUMBER: PCT/FR96/00166
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301 APAPAPAGEVAPTPTTPTPQRTLPA 325
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; ORGANISM: Mycobacterium tuberculosis
US-09-132-528-3
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US-09-132-528-3
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| GENERAL INFOGRATION: | GARDER IN A PAPELICANT: MARCIAL, GAILES | APPLICANT: MARCIAL, GAILES | APPLICANT: MARCIAL, GAILES | APPLICANT: PESCHER, Pascale | APPLICANT: PESCHER, Pascale | APPLICANT: PESCHER, PASCALE | TITLE OF INVENTION: MYCOBACTERIAL PROTEINS, MICORORGANISMS PRODUCING THEM | TITLE OF INVENTION: TUBERCULOSIS | TITLE OF INVENTION: TUBERCULOSIS | TITLE OF INVENTION: TUBERCULOSIS | TITLE OF INVENTION: TUBERCULOSIS | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASONO | GASO
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100.0%; Score 1726; DB 4; Length 325;
Best Local Similarity 100.0%; Pred. No. 6.4e-127;
Matches 325; Conservative 0; Mismatches 0; Indels 0.
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                                                                                                                                                                                                                  Query Match
100.0%; Score 1726; DB 3;
Best Local Similarity 100.0%; Pred. No. 6.4e-127;
Matches 325; Conservative 0; Mismatches 0;
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; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-08-875-494-2
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US-09-599-366-2
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Patent No. 6335181
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                                                          301 APAPAPAGEVAPTPTTPPORTLPA 325
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US-08-875-494-2
                     301 APAPAPAGEVAPTPTTPORTLPA
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APPLICANT: MARCHAL, Gilles
APPLICANT: MARCHAL, Gilles
APPLICANT: MARCHAL, Gilles
APPLICANT: PESCHER, Pescale
APPLICANT: PESCHER, Pescale
APPLICANT: PESCHER, Pescale
APPLICANT: PROMAIN, Felix
TITLE OF INVENTION: MYCOBACTERIAL PROTEINS, MICORORGANISMS PRODUCING THEM
TITLE OF INVENTION: TUBERCHOSIS
TITLE OF INVENTION: TUBERCHOSIS
TITLE OF INVENTION: TUBERCHOSIS
TITLE OF INVENTION: TUBERCHOSIS
TITLE OF INVENTION: TUBERCHOSIS
TITLE OF INVENTION: TUBERCHOSIS
TITLE OF INVENTION NUMBER: 09/132,528
PRIOR FILING DATE: 1998-08-11
PRIOR FILING DATE: 1998-08-11
PRIOR FILING DATE: 1998-08-11
PRIOR FILING DATE: 1998-08-11
PRIOR FILING DATE: 1906-04-30
NUMBER OF SEQ ID NOS: 5
SEQ ID NOS: 5
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SEG ID NOS: 5
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MHQVDPNLTRRKGRLAALAIAAMASASLVTVAVPATANADPEPAPPVPTTAASPPSTAAA 60
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Best Local Similarity 100.0%; Pred. No. 6.4e-127;
Matches 325; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/09599366 Patent No. 6335181 GENERAL INFORMATION:
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US-09-599-366-3
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APPLICANT: MARCHAL, GILLES
APPLICANT: MARCHAL, GILLES
APPLICANT: MARCHAL, GILLES
APPLICANT: MARCHAL, GILLES
APPLICANT: PESCHER, PASCALE
APPLICANT: PESCHER, PASCALE
APPLICANT: BESCHER, PELIX
TITLE OF INVENTION: WYCOBACTERIAL PROTEINS, MICROORGANISMS PRODUCING THEM
TITLE OF INVENTION: WYCOBACTERIAL PROTEINS, MICROORGANISMS PRODUCING THEM
TITLE OF INVENTION: TUBERCHOLOSIS
TITLE OF INVENTION: TUBERCHOLOSIS
TITLE OF INVENTION: WHOBER: US/08/875,494
CURRENT APPLICATION NUMBER: US/08/875,494
CURRENT PELING DATE: 1995-02-01
PRIOR FILING DATE: 1995-02-01
PRIOR FILING DATE: 1995-02-01
WUMBER OF SEQ ID NOS: 4
SOFTWARE: PATCHIN VOY: 2.0
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Sequence 6, Application US/09510031A
Patent No. 6638518
GENERAL INFORMATION:
APPLICANT: Rathle, Joel
TITLE OF INVENTION: METHOD FOR INHIBITING INFLAMMATORY RESPONSES
FILE REPERENCE: 140.010 010
CURRENT APPLICATION NUMBER: US/09/510,031A
CURRENT FILING DATE: 2000-02-22
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100.0%; Score 1726; DB 4;
Best Local Similarity 100.0%; Pred. No. 6.4e-127;
Matches 325; Conservative 0; Mismatches 0;
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APPLICANT: PESCHER, Pascale
APPLICANT: POWALN, Felia
APPLICANT: ROMAIN, Felia
TITLE OF INVENTION: MYCOBACTERIAL PROTEINS, MICORORGANISMS PRODUCING THEM
TITLE OF INVENTION: AND THEIR USE FOR VACCINES AND FOR THE DETECTION OF
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 0660-0138-001V
CURRENT APPLICATION NUMBER: 02001-11-02
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PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-11
NUMBER OF SEQ ID NOS: 5
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llarity 100.0%; Pred. No. 6.4e-127;
Conservative 0; Mismatches 0;
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Patent No. 6676945
GENERAL INFORMATION:
APPLICANT: LAQUEYRERIE, Anne
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Best Local Similarity
Matches 325; Conserv
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LENGTH: 325
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Patent No. 6676945

GENERAL INFORMATION:
APPLICANT: LAQUEYRERIE, Anne
APPLICANT: ROMAIN: Pascale
APPLICANT: ROMAIN: Pelix
APPLICANT: ROMAIN: Pelix
TITLE OF INVENTION: MYCOBACTERIAL PROTEINS, MICORORGANISMS PRODUCING THEM
TITLE OF INVENTION: TUBRECLOSIS
TITLE OF INVENTION: AND THEIR USE FOR VACCINES AND FOR THE DETECTION OF
TITLE OF INVENTION: USGROUPH OF THE DETECTION OF
TITLE OF INVENTION: WORDER: US/09/985,372
CURRENT FILING DATE: 2001-11-02
PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 09/132,528

PRIOR FILING DATE: BARLIER FILING DATE: 1998-08-11

NUMBER: OF SEQUENCY.
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                                                                                                                                                                                                                       Length 325;
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100.0%; Pred. No. 6.4e-127;
ive 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: US 60/121,177
PRIOR FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 8
SEGTWARE: Patentin version 3.0
SEQ ID NO 6
LENGTH: 325
                                                                                                                                                  ) ORGANISM: Mycobacterium tuberculosis
US-09-510-031A-6
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US-09-985-372-2
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Best Local S:
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                                                                                                                                                                                                                             APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardick, Thomas S.
ITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER REALDED FORM

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Vex

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/818,111

FILING DATE: 13-MAR-1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.

REGISTRATION NUMBER: 31,392

REGISTRATION NUMBER: 31,392

REFERNICE/DOCKET NUMBER: 210121.417C

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION SEQ ID NO: 53:

SEQUENCE: CHARACTERISTICS:
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308 APAPAPAGEVAPTPTTPTPQRTLPA 332
                                                                                                                           Sequence 53, Application US/08818111
Patent No. 6338852
                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 332 amino acid
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
US-08-818-111-53
                                                                               RESULT 13
US-08-818-111-53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 PPAPATPVAPPPPAAANTPNAQPGDPNAAPPPADPNAPPPVIAPNAPQPVRIDNPVGGF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 PPAPATEVAPPPPAAANTPNAQPGDPNAAPPPADPNAPPPPVIAPNAPQPVRIDNPVGGF 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 SFALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPPVANDTRIVLGRLDQKLYASAEA 180
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100.0%; Score 1726; DB 3; Length 332;
Best Local Similarity 100.0%; Pred. No. 6.5e-127;
Matches 325; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                         APPLICANT: Read, Steven G.
APPLICANT: Read, Steven G.
APPLICANT: Realix, Yasir A.W.
APPLICANT: Campos-Netc, Antonio
APPLICANT: Campos-Netc, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Twardiat, Thomas S.
APPLICANT: Twardiatk, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 98104-7092
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Comparatible
OCREMATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                     5: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/ACATION WARE
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REJECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
SEQUENCE CHARACTERISTICS:
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                                                                            Sequence 53, Application US/08818112
Parent No. 6290969
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 332 amino acids
TYPE: amino acid
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Washington
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TOPOLOGY:
US-08-818-112-53
                                                                 US-08-818-112-53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 GVIGSPAANAPDAGPPQRWFVVWLGTANNPVDKGAAKALAESIRPLVAPPPAAPAPABP 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MHQVDPNLTRRKGRLAALAIAAMASASLVTVAVPATANADPEPAPPVPTTAASPPSTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 332;
                                                                                                                                                                                APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Wedvick, Thomas S.
APPLICANT: Twardik, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Compounds AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION:

ATTONNEY/AGENT INFORMATION:

NAME:

REGISTRATION NUMBER:

ATTONNEY/AGENT INFORMATION:

REGISTRATION NUMBER:

REGISTRATION NUMBER:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDLIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                Sequence 53, Application US/09072596; Patent No. 6458366; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                332 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 6300 Colum
CITY: Seattle
STATE: Washington
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                                      RESULT 15
US-09-072-596-53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 SFALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPPVANDTRIVLGRLDQKLYASAEA 187
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                                                                                                                                                                      Sequence 53, Application US/09056556
Patent No. 6350456
Patent No. 6350456
GENERAL INFORMATION:
APPLICANT: Need, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Oblion, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESSONDENCES: 241
CORRESSONDENCE SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STRYEE: Mashington
COUNTRY: USA
ZIP: 98104-7092
ZIP: 98104-7092
COMPUTER: IEM PC compatible
COMPUTER: BEN PC compatible
COMPUTER: PatentIN Release #1.0, Version #1.30
CURRENT AFPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION NUMBER: US/09/056,556
FILING DATE: O7-APR-1998
REGISTRATION:
ATTONNEY AGAIN INFORMATION:
REGISTRATION NUMBER: 31,332
REFERENCE/DOCKET NUMBER: 21011.457
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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308 APAPAGEVAPTPTTPTPQRTLPA 332
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Search completed: July 7, 2004, 18:24:52 Job time: 25.5 secs

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                                                                                                                                  earch time 42.5 Seconds (without alignments) 2380.406 Million cell updates/sec
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1. /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2. /cgn2_6/ptodata/1/pubpaa/PCT NEW PUB.pep:*
3. /cgn2_6/ptodata/1/pubpaa/PCT NEW PUB.pep:*
4. /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
5. /cgn2_6/ptodata/1/pubpaa/USO7_NEW PUB.pep:*
6. /cgn2_6/ptodata/1/pubpaa/DCTOF_PUBCOMB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-985-372-3
US-10-193-002-53
US-10-084-843-53
US-10-098-73ZA-41
US-09-985-372-4
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US-10-425-114-41545

US-10-437-963-13068

US-10-437-963-13068

US-10-437-963-13068

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US-10-437-963-189482

US-10-437-963-189383

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### ALIGNMENTS

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Publication No. US20040086523A1
GENERAL INFORMATION:
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APPLICANT: LAQUERERIE, Anne
APPLICANT: MARCHAL, Gilles
APPLICANT: PESCHER, Pascale
APPLICANT: PESCHER, Pascale
APPLICANT: PESCHER, PASCALE
APPLICANT: PESCHER, PASCALE
APPLICANT: ROMAIN, PELIX
TITLE OF INVENTION: MYCOBACTERIAL PROTEINS, MICORORGANISMS PRODUCING THEM
TITLE OF INVENTION: AND THEIR USF FOR VACCINES AND FOR THE DETECTION OF
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 0660-0138-0DIV
CURRENT APPLICATION NUMBER: US/09/985,372
CURRENT FILING DATE: EARLIER APPLICATION NUMBER: 09/132,528
PRIOR PILING DATE: EARLIER FILING DATE: 1998-08-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATENTIN VOY. 2.1
SEQ ID NO 3
LENGTH: 325
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241 GVIGSPAANAPDAGPPORWFVVWLGTANNPVDKGAAKALAESIRPLVAPPPAAPAPAREP 300
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                                                                               TDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFSDPSKPNGQIWT
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US-09-985-372-3
                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09985372 Publication No. US20030054008A1 GENERAL INFORMATION:
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US-09-886-349A-41 ; Sequence 41, Application US/09886349A

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APPLICANT: Skeiky, Yasir
APPLICANT: Reed, Steven
APPLICANT: Reeson, Mark
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-009070US
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Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Romald C.
Hendrickson, Romald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 332;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 1726; DB 12;
100.0%; Pred. No. 8.7e-106;
tive 0; Mismatches 0;
                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/886,349A
CURRENT FILING DATE: 2001-06-20
PRIOR PRILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2001-02-01
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO. 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          308 APAPAPAGEVAPTPTTPTPQRTLPA 332
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US-10-193-002-53
; Sequence 53, Application US/10193002
; Publication No. US20030135026A1
; GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Skeiky, Yasir A.W.
Dillon, Davin C.
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Matches 325, Conservative
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128 SFALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPPVANDTRIVLGRLDQKLYASAEA 187
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                        Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPES Floppy disk
MEDIUM TYPES Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Parentin Release #1.0, Version #1.30
CURRN APPLICATION DATA:
APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY/AGRY INPORMATION:
NAME: MARI, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1726; DB 14;
100.0%; Pred. No. 8.7e-106;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 53:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 APAPAPAGEVAPTPTTPTPQRTLPA 325
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; Sequence 41, Application US/10098732A
; Publication No. US20030175294A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 332 amino acids
TYPE: amino acid
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                                                                                                                                                                                           CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 325; Conservative
                                                                                                                                                                                                                                       COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 SFALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPPVANDTRIVLGRLDOKLYASAEA 187
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                                         COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 1726; DB 14; Best Local Similarity 100.0%; Pred. No. 8.7e-106; Matches 325; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                        APPLICATION UNMER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY, AGRNT INFORMATION:
NAME: MAKi, David J.
REGISTRATION VUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPAR: (206) 682-4900
TELEPAR: (206) 682-6031
INFORMATION FOR SEQ ID NO: 53:
                                                                                                                                                                                                       CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-501-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 53:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 APAPAPAGEVAPTPTTPTPQRTLPA 325
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Dillon, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
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Publication No. US20030143243A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 332 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
CITY: Seattle
STATE: Washington
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US-10-084-843-53
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ORGANISM: Mycobacterium tuberculosis
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US-09-985-372-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188 TDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFSDPSKFNGQIWT 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248 GVIGSPAANAPDAGFPQKWFVVWLGTANNPVDKGAAKALAESIRPLVAFPPAPAPAEFP 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GVIGSPAANAPDAGPPQRWFVVWLGTANNPVDKGAAKALAESIRPLVAPPPAPAPAFFF 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09985372
Publication No. US20030054008A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LAQUEYRERIE, Anne
APPLICANT: PESCHER, Pascale
APPLICANT: ROWAIN, Felix
TITLE OF INVENTION: AND THEIR USE FOR VACCINES AND FOR THE DETECTION OF
TITLE OF INVENTION: THERE USE FOR VACCINES AND FOR THE DETECTION OF
FILE REFERENCE: 0660-0138-0DIV
CURRENT APPLICATION NUMBER: US/09/985,372
CURRENT APPLICATION NUMBER: US/09/985,372
CURRENT APPLICATION NUMBER: US/09/985,372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MHQVDPNLTRRKGRLAALALAAAASASLVTVAVPATANADPEPAPPVPTTAASPPSTAAA
                                          APPLICANT: Brandon, Mark
APPLICANT: Guderian, Jeffrey
APPLICANT: Guderian, Jeffrey
APPLICANT: Corrixa Corporation
TITLE OF INVENTION: Hererolagous Fusion Protein Constructs Comprising of TITLE OF INVENTION: Leishmania Antigen
FILE RERERENCE: 0.44058-0.12010US
CURRENT APPLICATION NUMBER: US,003-04-29
PRIOR APPLICATION NUMBER: US 60/275,837
PRIOR APPLICATION NUMBER: US 60/275,837
NUMBER OF SEO ID NOS: 80
SOFTWARE: PATENTIN Ver. 2.1
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PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 1726; DB 14; Length 332; 100.0%; Pred. No. 8.7e-106; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                           , OTHER INFORMATION: Description of Artificial Sequence:DPEP US-10-098-732A-41
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                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
Matches 325; Conservative
                        APPLICANT: Skeiky, Yasir
APPLICANT: Brannon, Mar
                                                                                                                                                                                                                                                                                                     SEQ ID NO 41
LENGTH: 332
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US-09-985-372-4
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                                                                                                                             40 DPEPAPPVPTTAASPPSTAAAPPAPATFVAPPPPAAANTPNAQPGDPNAAPPPADPNAPP
                                                                                                                                                                                                                                         100 PPVIAPNAPQPVRIDNPVGGFSFALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPPV
                                                                                                                                                                                                                                                                                                                                            160 ANDTRIVLGRLDQKLYASAEATDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSG
                                                                                                                                                                                                                                                                                                                                                                                            121 ANDTRIVIGRIDOKLYASAEATDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSG
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                      Length 286;
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Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS
TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               280 AESIRPLVAPPPAPAPAPAPAPAPAPAGEVAPTPTTPTPQRTLPA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 AESIRPLVAPPPAPAPAPABPAPAPAPAPAGEVAPTPTTPTPQRTLPA 286
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COUNTRY: USA
ZIP: 98104-709
ZIP: 98104-709
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING RELEASE #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSER: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                 Score 1542; DB 10;
Pred. No. 9.3e-94;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
RMATION FOR SEQ ID NO: 350:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-Jul-2002
CLASSIPICATION: <a href="https://doi.org/10/10/193/">CLASSIPICATION: <a href="https://doi.org/">CLASSIPICATION: <a href="https://doi.org/">CLASSIPICATION: <a href="https://doi.org/">CLASSIPICATION DATE: <a href="https://doi.org/">OS/09/072,596</a>
FILING DATE: 05-MAY-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 350, Application US/10193002 Publication No. US20030135026A1 GENERAL INFORMATION:
89.3%; Scur-
100.0%; Pre
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Skeiky, Yasir A.W.
Dillon, Davin C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
ADDRESSEE: SEED a
                                                                            Matches 286; Conservative
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                                                Best Local Similarity
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TELECOMMUNICATION INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                      167 LGRLDQKLYASAEATDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEV 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KFSDPSKPNGQIWTGVIGSPAANAPDAGPPQRWFVVWLGTANNPVDKGAAKALAESIRPL 286
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                                                                                                                                                                                                  Gaps
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Skeiky, Yasir A.W.
Dillon, Davin C.
Campton, Raymond
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                ö
                                                                                                                                                           Length 652;
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ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
COMPUTER: P8104-7092
COMPUTER: TBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: Datentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 25-Feb-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               287 VAPPPAPAPAPAPAPAPAGEVAPTPTTPTPQRTLPA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     614 VAPPPAPAPAPAPAPAPAPAGEVAPTPTTPTPQRTLPA 652
                                                                                                                                                     86.8%; Score 1499; DB 14;
100.0%; Pred. No. 1.5e-90;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Maki, David J. REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
            TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 350:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 355, Application US/10084843 Publication No. US20030143243A1 GENERAL INFORMATION:
652 amino acids
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STATE: Washington
                                                                                                                                                                       Best Local Similarity 100.0
Matches 279; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
                                                                                                               US-10-193-002-350
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US-10-084-843-355
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; OTHER INFORMATION: Description of Artificial Sequence:tetra-fusion
US-09-287-849-10
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                                                                                                                                                                                                Length
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                                                                                                                                                                                           86.8%; Score 1499; DB 14;
100.0%; Pred. No. 1.5e-90;
live 0; Mismatches 0;
TELEPHONE: (206) 622-4900
INFORMATION FOR SEQ ID NO: 355:
SEQUENCE CHARACTERISTICS:
LENGTH: 622 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOCOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 355:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application US/09287849
Patent No. US20020009459A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                         Query Match
Best Local Similarity 100.(
Matches 279; Conservative
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583
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                                                                                                                                                                                                                                                                                                                                                                                               524 VPTTAASPPSTAARPPAPATPVAPPPPAAANTPNAQPGDPNAAPPPADPNAPPPVIAPN
                                                                                                                                                                                                                              107 APQPVRIDNPVGGFSFALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPPVANDTRIV
                                                                                                                                                                                                                                                    167 LGRLDQXLYASABEATDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEV
                                                                                                                                                                                                                                                                                                                              644 LGRLDQKLYASAEATDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEV
                                                                                                                                                          47 VPTTAASPPSTAAAPPAAATPVAPPPPAAANTPNAQPGDPNAAPPPADPNAPPPPVIAPN
                                                                                                                                                                                                                                                                                                                                                                       227 KFSDPSKPNGQIWTGVIGSPAANAPDAGPPORWFVVWLGTANNPVDKGAAKALAESIRPL
                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Reed, Steven G.
Skelky, Yasir A.W.
Dillon, Davin C.
Campos-Netc, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Romald C.
TITLE OF INVENTION: COOMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                        .
0
                                                                                    Length 802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Seattle
STATE: Washington
COUNTY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
COMPUTER: IBM PC COMpatible
COMPUTER: DAYSTEM: PC-DOS/MS-DOS
SOFTWARING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FTLING DATE: US-Jul-2002
CLASSIFICATION: CURNOWN>
                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                              287 VAPPPAPAPAPAPAPAPAPAGEVAPTPTTPQRTLPA 325
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APPLICATION NUMBER: US/09/072,596
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                  86.8%; Score 1499; DB 14;
100.0%; Pred. No. 1.9e-90;
iive 0; Mismatches 0;
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 209:
US-10-193-002-209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (206) 622-4900
TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 346, Application US/10193002
Publication No. US20030135026A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and
                                                                                                                            Matches 279; Conservative
                                                                                                         Best Local Similarity
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                                                                                          Query Match
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                                                                                              47 VPTTAASPPSTAAAPPAPATPVAPPPPAAANTPNAQPGDPNAAPPPADPNAPPPVIAPN
                                                            Gaps
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Cantoo Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TILLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS
                      ; DB 9; Length 802; 1.9e-90;
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STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                VAPPPAPAPAPAPAPAPAGEVAPTPTTPTPQRTLPA 325
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                                             Pred. No. 1.9
Mismatches
                          Score 1499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
KMATION FOR SEQ ID NO: 209:
SEQUENCE CHARACTERISTICS:
LENGTH: 802 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 209, Application US/10193002 Publication No. US20030135026A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 05-MAY-1998 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
               86.8%; SCOL
100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                              Conservative
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                                               Similarity
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US-10-193-002-209
                                             Best Local Sim.
Matches 279;
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107 APQPVRIDNPVGGFSFALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPPVANDTRIV
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Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                     Length 802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITETE: Searche
CITY: Searche
CONTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION SATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
STREET: 6300 COlumbia Center, 701 Fifth Avenue
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100.0%; Pred. No. 1.9e-90;
tive 0; Mismatches 0;
                          REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                              STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 214:
       REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 351, Application US/10084843; Publication No. US20030143243A1 GENERAL INFORMATION:
                                                                                                                                                                  LENGTH: 802 amino acids TYPE: amino acid
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Best Local Similarity 100.0
Matches 279; Conservative
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US-10-084-843-214
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US-10-084-843-214
iS-10-084-843-214
sequence 214, Application US/10084843
publication No. US2003014324341
sephication No. US2003014324341
sephication No. US2003014324341
sephication No. US2003014324341
shell CANT: Reed, Steven G.
Dillon, Davin C.
Campos Neto, Autonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael N.
Hendrickson, Rohald C.
Hendrickson, Rohald C.
Hendrickson, Rohald C.
ALD DIAGNOSIS OF TUBERCULOSIS
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ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VAPPPAPAPAPAPAPAPAGEVAPTPTTPORTLPA 325
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATE:
FILING DATE: 25-Feb-2002
CLASSIFICATION: UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
BLING DATE: 05-MAY-1998
ATTORNEY/AGBNT INFORMATION:
NAME: Maki, David J.
                                                                                                                                     MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 346:
US-10-193-002-346
INFORMATION FOR SEQ ID NO: 346:
SEQUENCE CHARACTERISTICS:
LENGTH: 802 amino acids
                                                                    TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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STATE: Washington
COUNTRY: USA
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APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Netco, Antonic
APPLICANT: Campos-Netco, Antonic
APPLICANT: Campos-Netco, Antonic
APPLICANT: Campos-Netco, Antonic
APPLICANT: Campos-Netco, Antonic
APPLICANT: Campos-Netco, Antonic
APPLICANT: Corixa Corporation
ITILE OF INVENTION: and Their Uses
ITILE OF INVENTION: and Their Uses
FILE REFERENCE: 014058-003003
CURRENT APPLICATION NUMBER: US(10/259,460)
CURRENT APPLICATION NUMBER: US 08/918,112
PRIOR APPLICATION NUMBER: US 08/918,112
PRIOR FILING DATE: 1997-10-01
PRIOR FILING DATE: 1997-10-01
PRIOR APPLICATION NUMBER: US 09/056,556
FRIOR FILING DATE: 1998-12-30
FRIOR FILING DATE: 1998-12-30
FRIOR FILING DATE: 1998-12-30
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Best Local Similarity 100.0%; Pred. No. 1.9e-90;
Matches 279; Conservative 0; Mismatches 0; Indels 0
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APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MX-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFA: (206) 622-4900
TELEFA: (206) 622-4900
TELEFA: (206) 82-6031
INFORMATION FOR SEQ ID NO: 351:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 351:
US-10-084-843-351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10, Application US/10359460 Publication No. US20030147911A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                 LENGTH: 802 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
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US-10-359-460-10
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                                                                                                                                                                                                                                         524 VPTTAASPPSTAAAPPAAPTPVAPPPPAAANTPNAQPGDPNAAPPPADPNAPPPVIAPN
                                                                                                                                                                                                                                                                              107 APQPVRIDNPVGGFSFALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPPVANDTRIV
                                                                                                                                                                                                                                                                                                     227 KFSDPSKPNGQIWTGVIGSPAANAPDAGPPQRWFVVWLGTANNPVDKGAAKALAESIRPL
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                                                                                                                                                                                                                                                                                                                                                                            644 LGRIDOKLYASAEATDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEV
                                                                                                                                                                                Gaps
                                                                                   ) FEATURE:
, OTHER INFORMATION: Description of Artificial Sequence:tetra-fusion
US-10-359-460-10
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                                                                                                                                               802;
                                                                                                                                               Length
                                                                                                                                                                                Indels
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86.8%; Score 1499; DB 14;
Best Local Similarity 100.0%; Pred. No. 1.9e-90;
Matches 279; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: July 7, 2004, 18:33:33
Job time : 44.5 secs
                                                  TYPE: PRT
ORGANISM: Artificial Sequence
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
LENGTH: 802
                                                                                                                                                Query Match
Best Local Similarity
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                 protein search, using sw model
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US-10-720-192-3 1726 1 MHQVDPNLTRRKGRLAALAI.......PAGEVAPTFTTPTFQRTLFP 325

1586107 segs, 282547505 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched:

1586107 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

A Geneseq 29Jan04:\* Database :

genescap1980s: genescap2000s: genescap2001s: genescap201s: genescap2003s: genescap2003ss: genescap2003ss: geneseqp2004s:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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|-----------|----------------|--------------------|-------|------|------|------|-------------|----------|-------|-------------|-------|-------------|----|------|-------------|------|-------------|-------------|-----|-------------|-------------|-------------|-------------|-------------|----------|----------|
| SUMMARIES | De             | AAW03565           | 2     | 0    | œ    |      | AAW81683 Aa | AAY38945 |       | AAU01895 Aa |       | AAE17584 Aa | -  |      | AAY39082 Aa |      | AAW64379 Aa | AAW81746 Aa | e.  | AAY39033 Aa | AAY39081 Aa | AAY39176 Aa | AAY39224 Aa | AAU74592 Aa | ADB74347 |          |
|           | DB             | ; `                |       |      |      | 7    |             |          |       | ·           | ·     |             |    |      |             |      | •           |             |     | •           | •           |             | ·           | ·           |          | ,        |
|           | Length         | ı N                | N     | ന    | ന    | 332  | ന           | ന        | m     | m           | m     | ന           | N  | α    | ß           | IJ   | 802         | 0           | 0   | $\circ$     | 0           | 0           | 0           | 802         | ω        | u        |
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|           | Score          | 1726               | 1726  | 1726 | 1726 | 1726 | 1726        | 1726     | 1726  | 1726        | 1726  | 72          | 72 | 1542 | 49          | σ    | 4           | σ           | 4   | 49          | 49          | 49          | 1499        | 9           | œ        | 237 5    |
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| . E       |          | nam da   |          | Arabidops | Human pro | Protein e | Drosophil | Herbicida | Human mam | Mycobacte | Нитап тап | Human mam | mam mam  | Protein s | mam m    |          |          |          | n mam    |
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| Himan     |          |          | S        |           |           |           |           |           |           |           | Ниша      | Huma      |          |           | Human    |          |          |          | Human    |
| Ab1152945 | Abu52944 | Abu52939 | Abu0848' | Aaq15453  | Adb65210  | Abu37030  | Abb70063  | Abb92424  | Abu52938  | Aaw31852  | Abu52933  | Abu52931  | Abu52937 | Abr53281  | Abu52940 | Abu52936 | Abu52933 | Abq27250 | Abu52941 |
| ABU52945  | ABU52944 | ABU52939 | ABU08487 | AAG15453  | ADB65210  | ABU37030  | ABB70063  | ABB92424  | ABU52938  | AAW31852  | ABU52932  | ABU52931  | ABU52937 | ABR53281  | ABU52940 | ABU52936 | ABU52933 | ABG27250 | ABU52941 |
| 4         | 4        | 4        | φ        | 'n        | 7         | 9         | 4         | Ŋ         | 4         | 7         | 4         | 4         | 4        | ø         | 4        | 4        | 4        | 4        | 4        |
| 256       | 262      | 270      | 8991     | 544       | 652       | 598       | 446       | 652       | 267       | 763       | 260       | 267       | 253      | 817       | 261      | 277      | 254      | 406      | . 258    |
| 3.6       | 3.5      | 3,5      | 13.5     | .2        | .2        | 2.5       | 3.1       | 0.        | 12.9      | 9         | 8         | 8.        | 12.7     | 9.        | 9.       | 9.       |          | 4.       | 2.3      |
| H         | H        | H        | H        | H         | H         | H         | H         | ä         | H         | H         | H         | H         | ਜ        | Η         | H        | Ξ        | 1        | ä        | ä        |
| 235       | 233.5    | 233      | 233      | 228       | 227.5     | 227       | 225.5     | 223.5     | 222.5     | 222       | 221.5     | 221.5     | 218.5    | 217.5     | 217      | 217      | 216.5    | 214      | 212.5    |
| 26        | 27       | 28       | 53       | 30        | 31        | 32        | 33        | 34        | 35        | 36        | 37        | 38        | 39       | 40        | 41       | 42       | 43       | 44       | 45       |

# ALIGNMENTS

AAW03565 standard; protein; 325 AA. AAW03565; RESULT 1 **AAW03565** 

(first entry) 22-APR-1997

Mycobacterium tuberculosis antigenic determinant protein.

Antigenic determinant, Mycobacterium tuberculosis, ion exchange, human, chromatography; gel filtration; reverse phase column chromatography; immunogenic; serum; guinna pig; expression vector; cosmid; antibody; Mycobacterium smegmatis; Mycobacterium bovis BCG; microorganism; vaccine; hybrid; epitope; disease; diphtheria; cholera; toxin. 

Mycobacterium tuberculosis.

1. .39 /note= "signal peptide" /note= "mature protein" Location/Qualifiers .325 Key Peptide Protein

WO9623885-A1 08-AUG-1996

95US-00382184. 96WO-FR000166 31-JAN-1996; 01-FEB-1995; (INSP ) INST PASTEUR

Laqueyrerie A, Marchal

Romain F; Pescher P, Ġ WFI; 1996-371433/37. N-PSDB; AAT39357. Mycobacterium tuberculosis antigen and hybrid proteins comprising it useful in vaccines against tuberculosis and in immunoassays.

Claim 2; Page 49-50; 74pp; French.

This is the amino acid sequence of an antigenic determinant protein from Mycobacterium tuberculosis. The mature protein has calculated mol. wt. of 28779 Da but has an experimental mol. wt of 45-47 kD as determined by SDS -PAGE. The difference is thought to be due to the high frequency of Pro

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residues (21.7%) in the sequence. The protein was purified from M. tuberculosis strain H73Rb by conventional chromatographic methods e.g. low pressure ion exchange chromatography, Si 300 gel filtration, DEAE ion exchange and reverse phase column chromatography. The proteins were then separated by SDS-PAGE and immunogenic proteins determined with immune complex of mol. wt. 45-47 kD was identified. An expression library of genomic M. tuberculosis. A complex of mol. wt. 45-47 kD was identified. An expression library of genomic M. tuberculosis DN was generated in the cosmid vector pYUB18. The library was transformed inco M. smegnatis. Clones expressing antigenic determinants were isolated by screening with an antibody against the M. contained identical sequences i.e. the sequence presented here. The protein or microorganisms expressing it can be used as vaccines against tuberculosis. Also Mybrid proteins comprising this proteins and epitopes from other disease causing organisms or proteins, e.g. diphtheria or cholera toxin, can be used as vaccines against their respective diseases
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/label= Signal peptide
/note= "SEC-dependent signal secretion sequence"
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Matches 325; Conservative
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The present sequence is that of the Mycobacterium tuberculosis (Mtb) strain H71Rv gene Rv1860 product, designated ModD MT732. This is one of AAMS0729-59) discovered or cytocolic Mtb proteins of strain H31Rv (see AAMS0729-59) discovered through the use of 2-dimensional liquid phase electrophoresis coupled with an in vitro interferon-gamma assay and liquid chromatography-mass spectrometry. The immunogens stimulate a strong interferon-gamma response from T cells of M. tuberculosis infected mice. The invention provides vaccine compositions for boosting immunity to mycobacteria when administered in mid-life to a subject who has been vaccinated neonatally or in early childhood with BCG and in whom protective immunity has waned. The vaccine compositions comprise 1 or more of the 31 purified immunogenic proteins. When used as immunogens, the secreted Mtb proteins lack the secreted signal sequence. A preferred protein is Ag85A (see AAMS0759), the secreted product of the Rv3084v gene
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                                                                                                                                                                                                                       Vaccine for boosting immunity to mycobacteria when administered in mid-
life in a subject who has been vaccinated in childhood with Bacillus
Calmette-Guerrin, has purified proteins from mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                                               Claim 8; Page 17; 61pp; English.
10-JUL-2001; 2001WO-US021717.
                                           10-JUL-2000; 2000US-0217646P.
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Matches 325; Conservative
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Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant;

17-JAN-2002

us-10-720-192-3.rag

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AAW32418 standard; protein; 332

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                                                                                                                                                                                                                                                                                                       A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, DPEP. The immunogenic polypeptide can be used to diagnose M.tuberculosis infection by forming complexes with specific antibodies in the sample. Fragments of DNA encoding the immunogenic polypeptide can be used as diagnostic primers or probes and agence that bind to the antigen, especially monoclonal antibodies or equivalent polyclonal antibodies, are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GVIGSPAANAPDAGPPQRWFVVWLGTANNPVDKGAAKALAESIRPLVAPPPAPAPAPAPA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MHQVDPNLTRRKGRLAALAIAAMASASLVTVAVPATANADPEPAPPVPTTAASPPSTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SFALPAGWVESDAAHFDYGSALLSKTTGDPPFFQQPPPVANDTRIVLGRLDQKLYASAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFSDPSKPNGQIWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPAPATPVAPPPPAAANTPNAQPGDPNAAPPPADPNAPPPPVIAPNAPQPVKIDNPVGGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SFALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPPVANDTRIVLGRLDQKLYASAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVIGSPAANAPDAGPPQRWFVVWLGTANNPVDKGAAKALAESIRPLVAPPPAAPABA
                                                                                                                                                                                                                                                       New immunogenic polypeptide(s) from soluble M. tuberculosis antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 332;
                                                                                                                                                                                            Houghton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                           Campos-Neto A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 1726; DB 2;
100.0%; Pred. No. 1.3e-104;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                for diagnosis of M. tuberculosis infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APAPAPAGEVAPTPTTPTPQRTLPA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APAPAGEVAPTPTTPTPQRTLPA 332
                                                                                                                                                                                                                                                                                     Example 1; Page 92-94; 190pp; English
                                                                                                                                                                                          Dillon DC,
DR;
                                                                                                     95US-00523435.
95US-00532136.
96US-00620280.
96US-00658800.
96US-00680573.
 skin testing; M.tuberculosis.
                                                                                    96WO-US014675
                      tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 325; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      also used for diagnosis
                                                                                                                                                                                        Skeiky YAW,
I, Twardzik
                                                                                                                                                                                                                        WPI; 1997-192904/17.
                                                                                                                                                                     (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                 N-PSDB; AAT91423
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 332 AA;
                     Mycobacterium
                                                                                                                 22-SEP-1995;
22-MAR-1996;
05-JUN-1996;
12-JUL-1996;
                                         WO9709429-A2
                                                                                 30-AUG-1996;
                                                             13-MAR-1997
                                                                                                                                                                                                    Vedvick TH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19
                                                                                                                                                                                         sg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68
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                                                                                                                                                                                                                                                                 useful
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A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, DPEP. The immunogenic protein, and fusion proteins containing one or more of the proteins of the proteins plus EART-6, are useful in vaccines, preferably when formulated with a non-specific adjuvant, to induce an immune response against M.tuberculosis (for treatment or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVIGSPAANAPDAGPPORWFVVWLGTANNPVDKGAAKALAESIRPLVAPPPAPAPAPAEP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MHQVDPNLTRRKGRLAALAIAAMASASLVTVAVPATANADPEPAPPVPTTAASPPSTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 PPAPPATPVAPPPAAANTPNAQPGDPNAAPPPADPNAPPPPVIAPNAPQPVRIDNPVGGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 PPAPATPVAPPPPAAANTPNAQPGDPNAAPPPADPNAPPPPPVIAPNAPQPVRIDNPVGGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SFAL PAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPPVANDTRIVLGRLDQKLYASAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFSDPSKPNGQIWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New immunogenic polypeptide(s) from Mycobacterium tuberculosis - are useful in vaccines for prevention or treatment of tuberculosis, also diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MHQVDPNLTRRKGRLAALAIAAMASASLVTVAVPATANADPEPAPPVPTTAASPPSTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 SFALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPPVANDTRIVLGRLDQKLYASAEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Houghton R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1726; DB 2;
Pred. No. 1.3e-104;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Campos-Neto A,
                                             Mycobacterium tuberculosis antigen DPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 87-89; 168pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dillon DC,
DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Sc
100.0%; Pr
cive 0;
                                                                                                                                                                                                                                                                                                                                                                        95US-00523436.
95US-00533634.
96US-00620874.
96US-00659683.
                                                                                                                          testing; M.tuberculosis.
                                                                                                                                                                                                                                                                                                                             96WO-US014674
                                                                                                                                                                          Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 325; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Skeiky YA,
I, Twardzik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-192903/17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAT91486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                   22-SEP-1995;
22-MAR-1996;
05-JUN-1996;
12-JUL-1996;
                                                                                                                                                                                                                          WO9709428-A2
                                                                                                                                                                                                                                                                                                                             30-AUG-1996;
08-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                             01-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vedvick TH,
                                                                                                Antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
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121 SFALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPPVANDTRIVLGRLDQKLYASAEA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 PPAPATPVAPPPAAANTPNAQPGDPNAAPPPADFNAPPPPVIAPNAPQPVRIDNPVGGF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97WO-US018293
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 325; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-261042/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAV64498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-OCT-1996;
13-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9816646-A2
                                                                                                                                                                                                                                                                                                                                27-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reed SG, Sk
Vedvick TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-APR-1998,
                                                                                                                                                                                                                                                                                                    AAW81683;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This polypeptide comprises the Mycobacterium tuberculosis antigen DPEP. A bulb sequence (see AAV44390) coding for DPEP was isolated from a M. tuberculosis genomic library using a probe based on an isolated N-terminal peptide (see AAW64447). The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAW64491-W64319) comprising an antigenic portion of a soluble M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis in frection in a patient using these polypeptides, antibodies or oligonucleotide probes and primers, for the diagnosis of tuberculosis oligonucleotide probes and primers, for the diagnosis of tuberculosis. (Updated on 17-OCT-2003 to standardise OS field)
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GVIGSPAANAPDAGPPQRWFVVWLGTANNPVDKGAAKALAESIRPLVAPPPAAPAPAEP 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 PPAPATPVAPPPPAAANTPNAQPGDPNAAPPPADPNAPPPPVIAPNAPQPVRIDNPVGGF 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 PPAPATPVAPPPPAAANTPNAQPGDPNAAPPPADPNAPPPPVIAPNAPQPVRIDNPVGGF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MHQVDPNLTRRKGRLAALAIAAMASASLVTVAVPATANADPEPAPPVPTTAASPPSTAAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 MHQVDPNLTRRKGRLAALAIAAMASASLVTVAVPATANADPEPAPPVPTTAASPPSTAAA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated Mycobacterium tuberculosis polypeptides and DNA - used to develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dillon DC, Campos-Neto A, Houghton R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 1726; DB 2; Length 332; Best Local Similarity 100.0%; Pred. No. 1.3-104; Matches 325; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                         Tuberculosis; infection; diagnosis; antigen; DPEP.
                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis; strain H37Rv
                                                                                                                                                                                                                               Mycobacterium tuberculosis antigen DPEP.
                             APAPAPAGEVAPTPTTPORTLPA 325
                                                     308 APAPAPAGEVAPTPTTPTPORTLPA 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 93-94; 250pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vedvick TS, Twardzik DR, Lodes MJ;
                                                                                                                             AAW64322 standard; protein; 332 AA
                                                                                                                                                                                                                                                                                                                                                                         97WO-US018214.
                                                                                                                                                                                                                                                                                                                                                                                                       96US-00729622
                                                                                                                                                                                                                                                                                                                                                                                                                    97US-00818111
                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                      (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-251292/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAV44390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 332 AA;
                                                                                                                                                                                                                                                                                                                                                                         07-OCT-1997;
                                                                                                                                                                                                                                                                                                                  W09816645-A2
                                                                                                                                                                                                                                                                                                                                                                                                       11-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                   13-MAR-1997;
                                                                                                                                                                                   17-OCT-2003
09-NOV-1998
                                                                                                                                                         AAW64322;
 248
                             301
                                                                                                                 AAW6432
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This sequence represents an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the diagnosis of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
128 SFALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPPVANDTRIVLGRLDQKLYASAEA 187
                                                                                                                                                                                                                                                                    241 GVIGSPAANAPDAGFPQRWFVVWLGTANNPVDKGAAKALAESIRPLVAPPPAPAPAFAFF 300
                                                                                                                                                                                                                                                                                                                                               248 GVIGSPAANAPDAGPPQRWFVVWLGTANNPVDKGAAKALAESIRPLVAPPPAPAPAPAEP 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MHQVDPNLTRRKGRLAALAIAAMASASLVTVAVPATANADPEPAPPVPTTAASPPSTAAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67
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                                                                                                               181 IDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFSDPSKPNGQIWT
                                                                                                                                                                                      188 TDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFSDPSKPNGQIWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 MHQVDPNLTRRKGRLAALAIAAMASASLVTVAVPATANADPEPAPPVPTTAASPPSTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tuberculosis, immunogenic, soluble, antigen, protective immunity, TB, vaccine, pharmaceutical, infection, diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Campos-Neto A, Houghton R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1726; DB 2;
100.0%; Pred. No. 1.3e-104;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M. tuberculosis immunogenic polypeptide DPEP.
                                                                                                                                                                                                                                                                                                                                                                                                                             301 APAPAPAGEVAPTPTTPQRTLPA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       308 APAPAGEVAPTPTTPORTLPA 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 91-92; 230pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eiky YAW, Dillon DC, Ca
Twardzik DR, Lodes MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW81683 standard; protein; 332 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96US-00730510.
97US-00818112.
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240

SFALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPPVANDTRIVLGRLDQKLYASAEA 180

PPAPATPVAPPPAAANTPNAQPGDPNAAPPPADPNAPPPPVIAPNAPQPVRIDNPVGGF

68 121

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307

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This invention describes novel recombinant antigens and their encoding nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity
                           TDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFSDPSKPNGQIWT
                                            SFALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPVANDTRIVLGRLDQKLYASAEA
                                                                             GVIGSPAANAPDAGPPQRWFVVWLGTANNPVDKGAAKALAESIRPLVAPPPAPAPAEF
                                                                                             Antigen; diagnosis; detection; infection; antibody; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polypeptide comprising antigenic portions of M. tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Campos-Neto A, Houghton
J, Hendrickson RC;
                                                                                                                                                                                                                                                                                                M. tuberculosis recombinant antigen protein DPEP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 1726; DB 2;
100.0%; Pred. No. 1.3e-104;
ilve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 131-132; 323pp; English.
                                                                                                                               301 APAPAPAGEVAPTPTTPTPQRTLPA 325
                                                                                                                                                       308 APAPAPAGEVAPTPTTPTPORTLPA 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dillon DC, Car
DR, Lodes MJ,
                                                                                                                                                                                                                          Ā
                                                                                                                                                                                                                     AAY38945 standard; protein; 332
                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US003265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-00024753
98US-00072596
                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 325; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-527416/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAZ19088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 332 AA;
                                                                                                                                                                                                                                                                                                                                                                                         WO9942118-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                          17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reed SG, Sk
Vedvick TS,
                                                                                                                                                                                                                                                                         05-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                  26-AUG-1999.
  128
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                                                                                                                                                                                                                                                AAY38945;
                                                                                                                                                                                                                                                                                                                                        vaccine;
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127
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                                                                                                                   TDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFSDPSKPNGQIWT 240
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                                                                                                                                                                            241 GVIGSPAANAPDAGPPQRWFVVWLGTANNPVDKGAAKALAESIRPLVAPPPAPAPAEP 300
                                                                             248 GVIGSPAANAPDAGPPQRWFVVWLGTANNPVDKGAAKALAESIRPLVAPPPAPAPAPAP 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's. Macoines to protein containing M. tuberculosis Ag's. DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or tuberculosis to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion by, T, B or natural killer cells and/or macrophages in tuberculosis-immune subjects. AAZ1949 to AAX19460 and AAX199083 to AAX39225 are used in the exemplification of
                          PPAPATPVAPPPPAAANTPNAQPGDPNAAPPPADPNAPPPPVIAPNAPQPVRIDNPVGGF
                                                                                                                                              TDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFSDPSKPNGQIWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       skin
                                                        SFALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPPVANDTRIVLGRLDQKLYASAEA
 PPAPATPVAPPPPAAANTPNAQPGDPNAAPPPADPNAPPPPVIAPNAPQPVRIDNPVGGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful in diagnostic or compositions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis, M. tuberculosis, antigen; immunogen; immunotherapy; diagnosis; immunisation; vaccine; infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Houghton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Campos-Neto A, Ho
J, Hendrickson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                    M. tuberculosis antigen DPEP amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antigens from Mycobacterium tuberculosis tests and protective or therapeutic vaccines
                                                                                                                                                                                                                                        301 APAPAGEVAPIPITPIPORTLPA 325
                                                                                                                                                                                                                                                           Skeiky YAW, Dillon DC, Car
3, Twardzik DR, Lodes MJ,
                                                                                                                                                                                                                                                                                                                                             AAY39083 standard; protein; 332 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 93; 299pp; English.
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98US-00072967,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US003268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immune response; skin test.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-527409/44.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAZ19300.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9942076-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                      05-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-AUG-1999
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 61
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                                                                                                                                                                                                                                                                                                                                                                            AAY39083;
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Sequence 332 AA;

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Gaps

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Indels

1.3e-104;

Length 332;

MHQVDPNLTRRKGRLAALAIAAMASASLVTVAVPATANADPEPAPPVPTTAASPPSTAAA

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patients with acquired immunodeficiency disease, AIDS

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120
                                                                                                                                                            69 PPAPATPVAPPPPAAANTPNAQPGDPNAAPPPADPNAPPPPVIAPNAPQPVRIDNPVGGF 127
                                                                                                                                                                                                                                                                                                                                                                         248 GVIGSPAANAPDAGPPQRWFVVWLGTANNPVDKGAAKALAESIRPLVAPPPAPAPAFBE 307
                                                                                                                                                                                                             SFALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPPVANDTRIVLGRLDQKLYASAEA 180
                                                                                                                                                                                                                                  181 TDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFSDPSKPNGQIWT 240
                                                                                                                                                                                                                                                                                                                                                    GVIGSPAANAPDAGPPQRWFVVWLGTANNPVDKGAAKALAESIRPLVAPPPAAPAPAEP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence represents Mycobacterium tuberculosis DPEP, an M. tuberculosis antigen. Compositions comprising at least 2 heterologous antigens, as a fusion protein, and vectors expressing the fusion proteins are used as vaccines to prophylactically immunise mammals (especially minans) against infection by Mycobacteria. The compositions contein at least 2 heterologous antigens that increase the serological sensitivity of individuals infected with tuberculosis, a disease frequently affecting
                                                                     9
                                                                                                     67
                                                                     1 MHQVDPNLTRRKGRLAALAIAAMASASLVTVAVPATANADPEPAPPVPTTAASPPSTAAA
                                                                                            8 MIQVDPNLTRRKGRLAALAIAAMASASLVTVAVPATANADPEPAPPVPTTAASPPSTAAA
                                                                                                                                                                                                                                                                                                                 TDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFSDPSKPNGQIWT
                                                                                                                                         PPAPATTPVAPPPPAAANTPNAQPGDPNAAPPPADPNAPPPPVIAPNAPQPVRIDNPVGGF
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vaccinating against Mycobacteria infections in mammals using fusion proteins comprising combinations of heterologous antigens.
                                   ٠,
Query Match 100.0%; Score 1726; DB 2; Length 332; Best Local Similarity 100.0%; Pred. No. 1.3e-104; Matches 325; Conservative 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dillon DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mcneill PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DPBP; antigen; vaccine; tuberculosis; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   308 APAPAGEVAPTPTTPORTLPA 332
                                                                                                                                                                                                                                                                                                                                                                                                                        301 APAPAPAGEVAPTPITPORTLPA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 160; 168pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU01895 standard; protein; 332 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acquired immunodeficiency disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Skeiky Y, Reed S, Houghton RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M. tuberculosis DPEP antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-OCT-2000; 2000WO-US028095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0158338P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-290576/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                 241 GVIGSPAANAPDAGPPQRWFVVWLGTANNPVDKGAAKALAESIRPLVAPPPAPAPAFBF 300
                                                                                                                                                                                                                                                                                                                                                                                                                                     248 GVIGSPAANAPDAGPPORWFVVWLGTANNPVDKGAAKALAESIRPLVAPPAAPAPAPAED 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, MIS or 6H polynuclectide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis.
                                                                                                                                                                                                                      68 PPAPATPVAPPPPAAANTPNAQPGDPNAAPPPADPNAPPPPVIAPNAPOPVKIDNPVGGF 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a hererologous polynucleotide sequence encoding an antigen or an antigenic fragment from Mycobacterium sp. and a Leishmania polynucleotide sequence encoding a
                                                                                                           9
                                                                                                                                                                                                                                                                                       128 SFALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPFVANDTRIVLGRLDQKLYASABA
                                                                                                           1 MHQVDPNLTRRKGRLAALAIAAMASASLVTVAVPATANADPEPAPPVPTTAASPPSTAAA
                                                                                                                                                                                  61 PPAPATPVAPPPPAAANTPNAQPGDPNAAPPPADPNAPPPPVIAPNAPQPVRIDNPVGGF
                                                                                                                                                                                                                                                             121 SFALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPPVANDTRIVLGRLDQKLYASAEA
                                                                                                                                                                                                                                                                                                                                                                          188 IDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFSDPSKPNGQIWT
                                                                                                                                           8 MHQVDPNLTRRKGRLAALALAAMASASLVTVAVPATANADPEPAPPVPTTAASPPSTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vaccine; immunity; diagnostic agent; gene therapy; DPEP antigen.
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                                  Length 332;
                                                                      Indels
                              100.0%; Score 1726; DB 4;
100.0%; Pred. No. 1.3e-104;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis DPBP antigenic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 APAPARAGEVAPTPTTPQRTLPA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              308 APAPAGEVAPIPITPIPORILPA 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Guderian J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE29720 standard; protein; 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-MAR-2002; 2002WO-US008223.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-MAR-2001; 2001US-0275837P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-JAN-2003 (first entry)
                                                                      Matches 325; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Skeiky Y, Brannon M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-759844/82.
                                                    Best Local Similarity
Sequence 332 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200272792-A2.
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                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
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a subject

Mycobacterium species, useful for eliciting immune response in

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polypeptide or its fragment. The Leishmania polynucleotide is selected are used in methods for eliciting immune response in mammals. They are useful as vaccines to elicit protective immunity against pathogenic microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polynucleotides. Fusion in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is M. tuberculosis DPEP antigenic protein
                                                                                                                                                                                                                                                   120
                                                                                                                                                                                                                                                                                                   180
                                                                                                                                                                                                                                                                           127
                                                                                                                                                                                                                                                                                                                           187
                                                                                                                                                                                                                                                                                                                                                   240
                                                                                                                                                                                                                                                                                                                                                                                             GVIGSPAANAPDAGPPQRWFVVWLGTANNPVDKGAAKALAESIRPLVAPPPAAPAPAEP 300
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                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fusion protein; antigen; serological sensitivity; immune response; tuberculosis; infection; vaccine; DPEP protein.
                                                                                                                                                                         0;
                                                                                                                                                   Length 332;
                                                                                                                                                                         Indels
                                                                                                                                               ; Score 1726; DB 5;
; Pred. No. 1.3e-104;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium species DPEP protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE17584 standard; protein; 332 AA
                                                                                                                                                 100.0%;
100.0%;
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2001US-0265737P.
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                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 325; Conservative
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                                                                                                                        Sequence 332 AA;
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01-FEB-2001;
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Composition comprising MTB39 antigen and MTB32A antigen from

WPI; 2002-147798/19

N-PSDB; AAD28355

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The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nucleotides encoding them and compositions comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase the serological sensitivity of sera from individuals infected with cuberculosis and methods for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention and treatment of tuberculosis infection. Sequences of the invention and treatment of tuberculosis infection. Sequences of the invention and prevention of Mycobacterium infection. In the diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the polymuclectides are useful as diagnostic tools in patients infected with Mycobacterium, in vitro and in vivo assays for detecting humoral antibodies or cell-mediated immunity against M. tuberculosis, for the diagnosis of an infection or monitoring of disease progression, as immunogens to generate or elicit a protective immune response in a patient and for raising anti-M. Tuberculosis antibodies in a non-human animal. Sequences of the invention are also used as vaccines MTB32A fusion proteins of the invention are useful as in vivo diagnostic and minal sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 intradermal skin test. The present sequence is Mycobacterium species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inflammation, inflammatory response, irritant, pathogen, treatment, T helper cell, lymphocyte; cell mediated immunity, skin allergy; hives, allergic rhinitis, conjunctivitis, hay fever; allergic gastroenteritis, asthma, bronchopulmoary aspergillosis; pollutant; respiratory tract infection.
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100.0%; Pred. No. 1.3e-104;
ive 0; Mismatches 0;
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                                               English
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                                           Page 127; 136pp;
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Best Local Similarity
Matches 325; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 332 AA;
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                                         Claim 9;
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                                                                                                                                                                                                                                                                                                                                                                                         A new method of treating an inflammatory response comprises administering an microbial polypeptide which is preferably a mycobacterial polypeptide. The method is particularly useful for treating or inhibiting a Th2 mediated inflammatory response. The inflammatory response is associated with a disease such as skin allergy, hives, allergic thinitis, conjunctivitis, hay fever, allergy, hives, allergic thinitis, specifically, the asthma is intrinsic, i.e. associated with an irritant (e.g., a pathogen causing a respiratory tract infection in a mammal, or an inhaled pollutant). The asthma may also be extrinsic, which includes allergic asthma, occupational asthma or allergic bronchopulmonary
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                                                                                                                                                                                                                                                                                    Inhibiting an inflammatory response in a mammal for treating skin allergy, allergic rhinitis, hay fever, or asthma comprises administering a microbial polypeptide.
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                                                                                                                                                                                                                                                                                                                                                            Claim 4; Fig 1; 52pp; English.
                                                                                                                                    99US-0121177P.
                                                                                                   22-FEB-2000; 2000WO-US004463
                                                                                                                                                                     (IOWA ) UNIV IOWA RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                        WPI; 2000-549237/50.
Mycobacterium bovis.
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Matches 324; Conserv
                                                                                                                                                                                                                                                         N-PSDB; AAA53822.
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                                  WO200048622-A2.
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                                                                  24-AUG-2000
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AAW03566 standard; protein; 286 AA

AAW03566

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셤 à g ð D 8 (first entry)

22-APR-1997

AAW03566;

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This is the amino acid sequence of the mature potion of an antigenic determinant protein from Mycobacterium tuberculosis. The mature protein has calculated mol. wt. of 28779 Da but has an experimental mol. wt of 45 - 47 kp as determined by SDS-PAGE. The difference is thought to be due to the high frequency of Pro residues (21.7%) in the sequence. The protein was purified from W. tuberculosis strain H37Rb by conventional conformatographic methods e.g. low pressure ion exchange chromatography. The proteins were then separated by SDS-PAGE and chromatography. The proteins were then separated by SDS-PAGE and chromatography. The proteins were then separated by SDS-PAGE and chromatography. The proteins determined with immune serum from humans with TB or ginned pigs infected with W. tuberculosis. A complex of mol. wt. 45-47 kb was identified. An expression library of genomic W. tuberculosis DNA was generated in the cosmid vector pyUB18. The library was transformed into M. Smegmatis. Clones expressing antigenic determinants were isolated by screening with an antibody against the W. bovis BCG 45/47 kb proteins. Sclones were isolated here. The protein or microorganisms expressing it can be used as vaccines against tuberculosis. Also hybrid proteins comprising this protein and epitopes from other disease causing organisms or proteins, e.g. diphtheria or cholera toxin, can be used as vaccines against their respective diseases
                                                                            Antigenic determinant, Mycobacterium tuberculosis, ion exchange; human, chromatography; gel filtration; reverse phase column chromatography; immunogenic; serum; guinnea pig; expression vector; cosmid; antibody; Mycobacterium smegmatis; Mycobacterium bovis BGG; microorganism; vaccine; hybrid; epitope; disease; diphtheria; cholera; toxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis antigen and hybrid proteins comprising it useful in vaccines against tuberculosis and in immunoassays.
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Mycobacterium tuberculosis antigenic determinant mature protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laqueyrerie A, Marchal G, Pescher P, Romain
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                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 286; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1996-371433/37.
N-PSDB; AAT39357.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 286 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9623885-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-AUG-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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g à Db

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The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fuelon protein containing M. tuberculosis Ag's. M. tuberculosis Ag's. DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion by, T, B or natural killer cells and/or macrophages in tuberculosis-immune subjects. AZ19240 and AXY39083 to AXY39225 are used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 APQPVRIDNPVGGFSFALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPPVANDTRIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47 VPTTAASPPSTAAAPPAPATPVAPPPPAAANTPNAQPGDPNAAPPPADPNAPPPPVIAPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGRLDQKLYASAEATDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEV
                                                                                                                                                                                                                                                                                            4ycobacterium tuberculosis; M. tuberculosis; antigen; immunogen;
immunotherapy; diagnosis; immunisation; vaccine; infection;
                                                                                                                                                                                                                                                        M. tuberculosis fusion protein TbF-8 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lon DC, Campos-Neto A,
Lodes MJ, Hendrickson
           VAPPPAPAPAPAPAPAPAGEVAPTPTTPQRTLPA
                                       VAPPPAPAPAPAEPAPAPAGEVAPTPTTPORTLPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86.8%; Score 1499; DB 2;
100.0%; Pred. No. 1.5e-89;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 37; Page 274-276; 299pp; English.
                                                                                                                                               ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dillon DC,
                                                                                                                                           AAY39225 standard; protein; 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ilarity 100.0%; P:
Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-00025197
98US-00072967
                                                                                                                                                                                                                                                                                                                                  immune response; skin test.
                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reed SG, Skeiky YAW, Dill
Vedvick TS, Twardzik DR,
                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-527409/44.
N-PSDB; AAZ19460.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 652 AA;
                                                                                                                                                                                                                  05-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                             WO9942076-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-FEB-1998;
05-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-AUG-1999
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                                                                                                                                                                               AAY39225;
           287
                                                 614
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181 SASYYEVKFSDPSKPNGQIWTGVIGSPAANAPDAGPPQRWFVVWLGTANNPVDKGAAKAL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47 VPTTAASPPSTAAAPPAPATPVAPPPPAAANTPNAQPGDPNAAPPPPADPNAPPPVIAPN 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KFSDPSKPNGQIWTGVIGSPAANAPDAGPPQRWFVVWLGTANNPVDKGAAKALAESIRPL 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        434 APQPVRIDNPVGGFSFALPAGWVESDAAHFDYGSALLSKTTGDPFFGQPPFVANDTRIV 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes novel recombinant antigens and their encoding nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 APQPVRIDNPVGGFSFALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPPVANDTRIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  374 VPTTAASPPSTAAAPPAPATPVAPPPAAANTPNAQPGDPNAAPPPADPNAPPPVIADN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGRLDQKLYASAEATDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYBV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KFSDPSKPNGQIWTGVIGSPAANAPDAGPPQRWFVVWLGTANNPVDKGAAKALAESIRPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                        Antigen; diagnosis; detection; infection; antibody; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polypeptide comprising antigenic portions of M. tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 652;
                                       AESIRPLVAPPRAPAPAPAPAPAPAPAGBVAPTTTTPTPQRTLPA 325
                                                               AESIRPLVAPPPAPAPAPAEPAPAPAPAGEVAPITITIPIPA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Houghton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Campos-Neto A, Ho
J, Hendrickson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1499; DB 2; I
Pred. No. 1.5e-89;
O: Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96.8%; Scor.
100.0%; Pred. No. ...
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 10; Page 320-321; 323pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dillon DC, Car
DR, Lodes MJ,
                                                                                                                                                                                                                                                                                    M tuberculosis fusion protein TbF-8.
                                                                                                                                                                           Ą.
                                                                                                                                                                           652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-00024753
                                                                                                                                                   AAY39082
ID AAY39082 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 279; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Skeiky YAW,
3, Twardzik
                                                                                                                                                                                                                                                (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1999-527416/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAZ19248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 652 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                 WO9942118-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-FEB-1998;
05-MAY-1998;
                                                                                                                                                                                                                                                05-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vedvick TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-AUG-1999
                                       280
                                                                           241
                                                                                                                                                                                                          AAY39082,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167
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Best Local
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Houghton R; RC;

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Gaps

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493 226 553

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227 KFSDPSKPNGQIWTGVIGSPAANAPDACPPQRWFVVMLGTANNPVDKGAAKALAESIRPL 286
                                  287 VAPPPAPAPAPABAPAPAPAPAGSVAPTPTTPTPQRTLPA 325
 8 6 6 6
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Search completed: July 7, 2004, 18:21:03 Job time: 50.5 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

July 7, 2004, 18:19:15; Search time 22.5 Seconds (without alignments) 1389.433 Million cell updates/sec Run on:

US-10-720-192-3 1726 I MHQVDPNLTRRKGRLAALAI.......PAGEVAPTPTTPTPQRTLPA 325 Title: Perfect score: Sequence:

283366 seqs, 96191526 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMADIES

|           | Description    |   | probable modD prot | ical   | ical prot | -like pro | - Volvox | hypothetical prote | tegument protein 2 | antigen 43L [impor | verprolin - yeast | hypothetical prote | _G     | hypothetical prote | extensin homolog T | e       | extensin-like cell | dermal gland prote | hypothetical prote | hypothetical prote | prot   | 367K tegument prot | hydroxyproline-ric | ical prot | proline-rich cell | Pto    | l prot | extensin homolog F | inding | מ      | hypothetical prote |  |
|-----------|----------------|---|--------------------|--------|-----------|-----------|----------|--------------------|--------------------|--------------------|-------------------|--------------------|--------|--------------------|--------------------|---------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|-----------|-------------------|--------|--------|--------------------|--------|--------|--------------------|--|
| SUMMARIES | ID             |   | D70666             | B87166 | T31611    | S49915    | S22697   | H96711             | T42567             | T44744             | S51342            | F75518             | T29018 | F96531             | T06291             | WMBEH6  | T10737             | SKXLAG             | T38236             | T28770             | G86441 | WZBEB6             | S13383             | H75457    | T09854            | F86387 | D96711 | T04859             | A47282 | T15142 | B70803             |  |
|           | DB             | 1 | Ŋ                  | Ŋ      | Ŋ         | ~         | 7        | 7                  | ~                  | 7                  | ~                 | N                  | ~      | ~                  | ~                  | Н       | ~                  | П                  | N                  | Ŋ                  | 7      | Н                  | 0                  | 7         | 7                 | 7      | ~      | ~                  | ~      | N      | N                  |  |
|           | Length         | } | 325                | 287    | 1585      | 1188      | 464      | 222                | 3534               | 92                 | 817               | 839                | 801    | 847                | 760                | 3164    | 214                | 416                | 1611               | 539                | 1201   | 3421               | 283                | 395       | 214               | 760    | 708    | 839                | 865    | 418    | 999                |  |
| d         | Query<br>Match |   | •                  | 'n     |           | ~·        | ~        | m                  | ~·                 | ٠.                 | ٠.                | ٠.                 | ٠.     | ٠.                 | ٠.                 | ٠.<br>ن | ~;                 | ٠.                 | ٠:                 | _;                 | _:     | _;                 | _:                 | _:        | :                 | :      |        |                    | 급.     |        | ij                 |  |
|           | Score          | - | 1726               | യ      | 24        | 37.       | 28.      | •                  | 24.                | 19.                | 17.               | 17.                | ~      | 16.                |                    | 13.     | 08.                | 20                 |                    | 04.                | 0      | 70                 | 02.                |           | 000               | 00     | J.     | Th.                | 97.    |        | 96.                |  |
|           | Result<br>No.  |   | rri                | 7      | m         | 4         | ហ        | 9                  | 7                  | ω                  | σ                 | 10                 | 11     | 12                 | 13                 | 14      | 15                 | 16                 | 17                 | 18                 | 19     | 20                 | 21                 | 22        | 23                | 24     | 25     | 26                 | 27     | 28     | 29                 |  |

| probable proline-r | hydroxyproline-ric<br>hypothetical prote<br>hypothetical prote | calphotin - fruit<br>extensin-like prot | probable serine/th | cell wall glycopro<br>proline-rich prote | hypothetical diver<br>proline-rich prote | US4 protein - huma | hydroxyproline-ric |
|--------------------|----------------------------------------------------------------|-----------------------------------------|--------------------|------------------------------------------|------------------------------------------|--------------------|--------------------|
| F84522<br>T18535   | SU6/33<br>T04455<br>E86255                                     | A47283<br>T11671                        | T36729<br>G70597   | S08314<br>B24264                         | T38459<br>T17547                         | C43674<br>T31420   | S22456             |
| 000                | 100                                                            | 0 0                                     | 0 0                | 2 2                                      | 7 7                                      | 010                | 7                  |
| 191                | 731                                                            | 873<br>280                              | 576<br>550         | 267                                      | 1794<br>544                              | 1268               | 350                |
| 11.2               | 11.2                                                           | 11.2                                    | 11.1               | 11.0                                     | 11.0                                     | 10.9               | 10.8               |
| 193.5              | 192.5<br>192.5                                                 | 192.5                                   | 191                | 189.5                                    | 189<br>188                               | 188                | 187                |
| 30                 | 1 (U (U<br>1 (U 4)                                             | 35<br>36                                | 37<br>38           | ы<br>Ф О                                 | 4 4<br>2 4 2                             | 4 4<br>4 4         | 45                 |

# ALIGNMENTS

| REBULT 1  PUDDAGE modD protein - Mycobacterium tuberculosis (strain H37RV)  PUDDAGE |
|-------------------------------------------------------------------------------------|
|-------------------------------------------------------------------------------------|

RESULT 2

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1435 PP------PPAPAPAPAPASGGYSGG--GSSGGSAAGGGGGSSGGYTGGSAAP--- 1478
                                                                                                                                                                                                                                                                                                                                                               --- AAGGGGGSSGGYSGGSAAPP 1434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 PFPGOPPVANDTRIVLGRLDOKLYASAEATDSKAAARLGSDWGEFYMPYPGTRINQETV 210
                                                                                                                                                                                                                                     KPNGQIWTGVIGSPAANAPDAGPPQRWFVVWLGTANNPVDKGAAKA----LAESIRPLVA 288
                                                                                                                                                                                                                                                                                                                         -----GEVAPTPTTPTPQ 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           271 VDKGAAKALAESIRPLVAPPPAP----APAPAE---PAPAPAGEVAPTFTTPTPQRTL 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         extensin-like protein - maize
()Species: Zea mays (maize)
()Species: Zea mays (maize)
()Species: Zea mays (maize)
()Accession: S4915
S.Rubinstein, A.L., Broadwater, A.H.; Lowrey, K.; Bedinger, P.A.
Submitted to the EMBL Data Library, June 1994
A,Description: Pex genes: pollen-specific genes with extensin-like domains.
A,Reference number: S49915
A,Accession: S49915
A,Actus: preliminary
A,Molecule type: DNA
A,Residues: 1-1188
A,Residues: 1-1188
A,Residues: I-1188
A,Cross-references: EMBL:Z34465; NID:g600117; PIDN:CAA84230.1; PID:g600118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPREPVSSPPQ---TPKSSPPAAPVSSPPATPVSSPPALAPVSSPPQ----SVKSSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 PATANADPEP--APPVPTTAASPPSTAAAPPAAATPVAPPPPAAANTPNAQPGDPNAAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         658 PAVASPPVKSPPPTLVASPPPVKSPPPAA-PVASPPPVKSPPPVKSPPPVASPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92 PADPNA-PPPVIAPNAPQPVRIDNPVGGFSFALPAGWVESDAAHFDYGSALLSKTTGDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               625 PPAPVASSPPPMKSP--PPTPVSSPPPPEKSPPPPAKSTPPPEEYPTPPTSVKSSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         211 SLDANGVSGSASYYEVKFSDPSKPNGQIWTGVIGSPAANAPDAGPPQRWFVVWLGTANNP
                                                                 113 IDNPVGGFSFALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPVANDTRIVLGRLDQ
                                                                                                                                                 173 KLYASAEATDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFSDPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1188;
                                                                                                      1351 SGGYSGGSSAGGGGGSSGGYTGGSA----APPPPPPPPPPPPPP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   683 PEKSLPPP----TLIPSPPPQEK--PTPPSTPSKPPS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
13.8%; Score 237.5; DB 2;
Best Local Similarity 28.9%; Pred. No. 8.2e-06;
Matches 87; Conservative 30; Mismatches 123;
                                                                                                                                                                                            ---APAPAPSSGGYSG-GSSGGS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   extensin - Volvox carteri (fragment)
C;Species: Volvox carteri
                                                                                                                                                                                                                                                                                                                               289 PPPAPAPAPAEPAPAPA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1539 PPPPA 1543
                                                                                                                                                                                                                                                                                                                                                                                                                   321 RTLPA 325
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                    hypothetical protein modD [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001
C;Accession: B87166
R; Davies, R.T.; Eigimeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hc
R; Davies, R.M.; Devlin, K.M.
Man, J. Rutherford, X.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A;Reference number: A86909; MUID:21128732; PMID:111234002
A;Accession: B87166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
T3161
hypothetical protein Y50E8A.g - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T31611
R;Steward, C
Submitted to the EMBL Data Library, September 1999
A;Recession: T31611
A;Accession: T31611
A;Accession: T31611
A;Accession: T31611
A;Residues: 1-1585 Ault-
A;Accession: T31611
A;Residues: 1-1585 Ault-
A;Cross-references: EMBL:AL117200, NID:e1549770; PIDN:CAB55050.1; CESP:Y50E8A.g
A;Cross-references: EMBL:AL117200, NID:e1549770; PIDN:CAB55050.1; A;Gene: CSSP:Y50E8A.g
A;Gene: CSSP:Y50E8A.g
A;Gene: CSSP:Y50E8A.g
A;Introns: 25/3; 60/1; 133/2; 217/3; 270/3; 337/2; 400/1; 746/2
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                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-287 <STO>
A;Cross-references: GB:AL450380; NID:gl3093663; PIDN:CAC31010.1; GSPDB:GN00147
C;Genetics:
A;Gene: modD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPPVANDTRIVLGRLDOKLYASAEA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFSDPSKPNGQIWT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 PPAPATPVAPPPPAAANTPNAQPGDPNAAPPPADPNAPPPPVIAPNAPQPVRIDNPVGGF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --TAAAPPAPATPVAPPPAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MHQVDPNLTRRKGRLAALALAAMASASLVTVAVPATANADPEPAPPVPTTAASPPSTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14; Gaps
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Best Local Similarity 26.6%; Pred. No. 7.1e-06;
Matches 97; Conservative 12; Mismatches 122; Indels 134
                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 66.8%; Pred. No. 8.8e-47;
Matches 199; Conservative 21; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 ANTPNAQPG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52
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| Db 28 AASPVTSTTTAPPPTTAAPPTTTTPPVSAAQPPASPVTPPPAVTPTSPPARKV 87  76 AN-TPNAQPGDENAAPPADENAPPPEVTAPPOPVRIDNPVGGFSFALPAGWVESDA 133  B                                                                                                                                                                                                                                                                                                                                                                                                                                                  | RESULT 7  tequine berpeavirus 4 (strain NS80567)  tequine berpeavirus 4 (strain NS80567)  C.Species: equine herpeavirus 4  C.Species: equine herpeavirus 4  C.Species: equine herpeavirus 4  C.Species: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000  R.Telford, E.A.; Matson, M.S.; Perry, J.; Cullinane, A.A.; Davison, A.J.  A.Tille: The DNA Sequence of equine herpeavirus 4.  A.Tille: The DNA Sequence of equine herpesvirus 4.  A.Tille: The DNA Sequence of equine herpesvirus 4.  A.Stetuence number: 222173; MUID:98264497; PMID:9603335  A.A.Cecssion: T42567  A.A.Cecssion: Taylor A.C.  A.A.Cecssion: T42567  A.C.    |
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| Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jul-2000 Accession: S22697; S21006 Ettl, H.; Hallmann, A.; Wenzl, S.; Sumper, M. BED J. 11, 2055-2062, 1992 Title: A novel extensin that may organize extracellular matrix biogenesis Reference number: S22697; MUID: 92289669; PMID:1600938 Accession: S22697 MOJECULE type: mRNA Residues: 1-464 < HAL> Cross-references: EMBL:X65165; NID:g21991; PIDN:CAA46283.1; PID:g21992 Reywords: glycoprotein 13.2%; Score 228.5; DB 2; Length 464; Best Local Similarity 22.3%; Pred. No. 16-06; Matches 34 PATANADPEPA | TTGDPPFPGOPPVANDTRIVLGRLDOKLYASAEATDSKAARR SPPPPSOPPPRABES                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |  |

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304 PAPAGEVAPTPTTPTP 319
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                                                                                                                                  F;421-445/Region: proline-rich
F;518-528/Region: proline-rich
F;608-621/Region: proline-rich
F;608-621/Region: proline-rich
F;649-661/Region: proline-rich
F;678-661/Region: proline-rich
F;704-710/Region: proline-rich
F;349-357/Region: proline-rich
F;372-382/Region: proline-rich
                                         proline-rich
proline-rich
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                                                                                         F;396-406/Region:
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F75518
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verpoin - yeast (Saccharomyces cerevisiae)
NyAlternate names: prolin-rich protein VRP1; protein L0300.13; protein VLR337c
C;Species Saccharomyces cerevisiae
C;Species Saccharomyces cerevisiae
C;Species Saccharomyces cerevisiae
C;Accession: S51342; S39626; S57435
R;Du, Z
submitted to the EMBL Data Library, December 1994
A;Bescription: The sequence of S. cerevisiae cosmid 8300.
A;Reference number: S51339
A;Accession: S51342
A;Molecule type: DNA
A;Residues: 1-817 cDUZ>
A;Molecule type: DNA
A;Residues: EMBL,U19028; NID:G609380; PID:G609392; MIPS:YLR337c
A;Gress-references: EMBL,U19028; NID:G609380; PID:G609392; MIPS:YLR337c
A;Accession: S5136.
A;Accession: S513626; Mulp: Protein, Worlved in cytoskeletal organization and ce
A;Accession: S39626
A;Reference number: S39626; Mulp:95058201; PMID:7968536
A;Accession: S39626
A;Accession: S39636
A;Accession:
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                                                                                                                   Cispecies: Mycobacterium inpression 11-Jan-2000 #text_change 21-Jan-2000 (Species: Mycobacterium inpression 21-Jan-2000 #text_change 21-Jan-2000 (Cispecies: Mycobacterium inpression 21-Jan-2000 #text_change 21-Jan-2000 (Cispecies: Mycobacterium inpression: 17-Jan-2000 #text_change 21-Jan-2000 Riparkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, October 1997 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Reference number: 228833 A;Refere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.7%; Score 219.5; DB 2; Length 85;
52.1%; Pred. No. 5.7e-06;
tive 8; Mismatches 27; Indels 11; Gaps
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A;Cross-references: EMBL:X87806; NID:g871534; PID:g871535
A;Experimental source: strain W303
C;Genetics:
                                                                                         antigen 43L [imported] - Mycobacterium leprae (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 PPARATPVAPPPRAAANTPNAQPGDPNAAPPADPN 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 APSPAQEIITPLPGAPVSSEAQPGDPNA--PSLDPN 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:AL008609; PIDN:CAA15433.1
A;Experimental source: cosmid B1788
C;Genetics:
A;Note: 43L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Gene: SGD:VRP1, MDP5, END5
A,Cross-references: SGD:S0004329, MIPS:YLR337c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 52.1%
Marches 50; Conservative
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F,216-245/Region: proline-rich
F,305-336/Region: proline-rich
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F,5-14/Region: proline-rich
F,77-85/Region: proline-rich
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hypothetical protein - Deinococcus radiodurans (strain R1)
(Species: Deinococcus radiodurans
(Species: Deinococcus radiodurans
(Species: Deinococcus radiodurans
(Species: O3-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
(Accession: F75518
(A. A. Falen, M.) Heidelberg, J.F.; Hickey, B.K.; Peterson, J.D.; Dodson, R.J.; F. W.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Maj. S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
(A. Sience 286, 1871-1877, 1999
(A. Fraser, Decension of the radioresistant bacterium Deinococcus radiodurans R1.
(A. Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-839 <WHI>
A;Cross-references: GB:AE001904; GB:AE000513; NID:g6458129; PIDN:AAF10038.1; PID:g645814:
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 PLFLSGASAPKVPQNRPHMPSVRPAHRSHQRKSSNISLPSVSAPPLPSASLPTHVSNPPQ 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 APPPPV-----IAP--NAPQPVRIDNPVGGFSFALPAGWVESDAAHFDYGS---- 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 -----ALLSKTTGDPPFPGQPPPVAND-----TRIVLGRLDQKLYASAEATDSKAAA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      293 SSTKIQTENHKSPSQPPLPSSAPPIPTSHAPPLPPTAPPPPSLPNVTSAPKKATSAPAPP 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 RLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFSDPSKPNGQIWTGVIGSPA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         393 SSMPAPPPPSVATSVPSALSASSIPLAPLPPPPSVATSVPSA 440
                                                                                                                                                                                                                                                                                                          118 ASAPPIPGAVPSVAAPPIPNAPLSPAPAVPSIPSSSAPPIPDIPSSAAPPIPIVPSSPAP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                353 P-----PPLPAAMSSASTNSVKATPVPPTLA-----PPLPN---TTSVPPNKA 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248 ANAPDAGPPQRWFVVWLGTANNPVDKGA---AKALAESIRPLVAPPPAAPAFPAPAFPA-A 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Superfamily: herpesvirus immediate-early protein IE110; RING finger homology
                                                                                                                                                                                                                24 ASASLVTVAVPATA----NADPEPAPPVPT--TAASPP----STAAAPPAPATVAPPP 72
                                                                                                                                                                                                                                                                                                                                                                                                                                22 AMASASLVTVAVPATANAD----PEPAP--PVPTTAASPPSTAAAP----PAPATPVAP- 70
Query Match 12.6%; Score 217.5; DB 2; Length 817; Best Local Similarity 26.3%; Pred. No. 6.9e-05; Matches 99; Conservative 31; Mismatches 125; Indels 121; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 12.6%; Score 217.5; DB 2; Length 839; Local Similarity 25.4%; Pred. No. 7.1e-05; Indels 131; Gaps 185; Conservative 24; Mismatches 124; Indels 131; Gaps
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| Qy 239 WTGVIGSPAANAPDAGPPORWEVVWLGTANNPVDKGAAKALAE 281<br>::                                                           | 282 SIRPIVAPPAARAPA-ARBABABABABABABTUTTTTTTTTTTTTTTTTTTTTTTT | 542 YDAPSSVPBETPAPAADETPAPAABETPAPAAETPAPA | RESULT 12 F96531 hypothetical protein F13F21.7 [imported] - Arabidopsis thaliana C.Species: Arabidopsis thaliana (mouse-ear cress) | C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: F96531 C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conn. L.; Conway, A.R.; Chung, M.K.; Conn. L.; Conway, A.R.; Croway, A.R.; Croway, A.R.; Conn. D.; Conway, A.R.; Croway, A.R.; Conway, A. | ansen, N.F.; Hughes, B.; Huizar, L.  Nature 408, 816-820, 2000  AyAuthors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.: Luros, J.S.: Mairi. R.; Marriali | Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Mu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome I of the plant Arabidopsis. A;Reference number. A86141. WITD. 31016219. | A.Accession: F96531 A.Status: preliminary A.Molecule type: DNA A.Residues: 1-847 <sto> A.Cross-references: GB:AE005173; NID:g5430752; PIDN:AAD43152.1; GSPDB:GN00141 C.Genetics: A.Gene: F13F21.7 A.Mon Dosition: 1</sto>                 | Query Match 12.5%; Score 216.5; DB 2; Length 847; Best Local Similarity 26.0%; Pred. No. 8.1e-05; Matches 79; Conservative 35; Mismatches 135; Indels 55; Gaps 12;                              | QY 33 VPATANADPEPAPPVTTAASPPSTAAAPPATPVAPPPPAAANTPNAQPGDPNA 88                                                                                                              | QY 89 APPPADENAPPPUTAPNAPQPVRIDNEVGGRSFALPAGWVESDAAHFDYGSALLSKTTG 148 | OGY;  QY 149 DPPFPGQPPVANDTRIVLGRLDQKLYASAEATDSKAAARLGSDMGEFYMPYPG-TRI 205                                                             |                                                                                                                                                                       | 263 WLGTANNPVDKGAAKALABSIRPLVAPPPAPAPAPAPAPAPAPAGEV-APTPT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | DD 739TPSSESNQSPSQAPTFILEPVHAPTFNSKPVQSPTPS-SEPVSSPEQSEEVEAPEPT 794 Qy 316 TPTP 319 | <br> <br> <br> <br> <br> <br>                      | RESULT 13 T06291 extensin homolog T9BB.80 - Arabidopsis thaliana C;Species: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-Jun-1999 C;Accession: T06291 R;Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Schuell 8;Reference number: Z15588 |
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| Db 91 APATKPTPTPAKPATPAPEPPKPPEPTPPEPKPETPPEPPKPAPEPPKPDFTPAEPLKPP 150 Qy 71PPVAANTPNAQPGDPNAAPPPADDNAPPPPVIAPNAPO 109 |                                                              |                                            |                                                                                                                                    | Qy         209 TVSLDANGVSGSASYYEVKFSDPSKPNGQIWTGVIGSPAANAPDAGPPORWFVVWLGTAN 268           DD         :     :     :                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | OY 269 NPUDKGAAKALAESIRPLVAPPPAPAPAPAPAPAPAPAPAPAPAPAPAP                                                                                                                                                                                         | Qy 306 PAGEVAPTPTTP 319<br>:                                                                                                                                                                                                                                                                                                 | RESULT 11<br>T29018<br>hypothetical protein ZK84.1 - Caenorhabditis elegans<br>C:Species: Caenorhabditis elegans<br>C;Decies: IS-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000<br>C;Accession: T29018<br>R;Kirsten, J. | omitteed to the EMBL Data Library, April 1995 Description: The sequence of C. elegans cosmid ZK84. Reference number: 220553 Accession: T29018 Status: prelimitary: translated from GB/DMBL/Anbl | Molecule type: DNA. Residues: 1-801 <ktr> Cross-references: EMBL:U23181; PIDN:AAC48204.1; GSPDB:GN00020; CESP:ZX84.1 Experimental source: strain Brietol N. Clone Yes</ktr> | Genetics: CSPE xR84.1<br>Map position: 22/2; 45/3; 108/1              | Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology Query Match  12.6%; Score 217; DB 2; Length 801; | <pre>Best Local Similarity 24.2%; Pred. No. 7.2e-05; Matches 101; Conservative 37; Mismatches 151; Indels 116; Gaps 16; Qy 25 SASLVIVAVPATANADPEPAPPVPTTAASPPST</pre> | Db 194 ASGYVTSEQEQGAGDAPEPAPVVEETPAPTPAARETPAPATEASNAVGTPEGYVDGTANA 253 OV 58 AAADDADATDAABANTD-NAADGODNAAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTAAGGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAGDGAANTD-NAAG | 254                                                                                 | QY 115 NPVGGFSFALPAGWVESDAAHFDYGSALLSKTTGD 149<br> | 150 -PPFPGQPPPVANDTRIVLGRLDQKLYASAEATDSKAAARLGSDMGEF 371 TTPABSVPAFVADAAAGYDSPSSIPETPAPAAEDTPAPAAAAEETPAPAABE 197 YMPYPGTRINQETVSLDANGVSGSASYYEVKFSDPSKPNGQI 6                                                                                                                           |

| QY         171 DQKLYASABATDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFSD 230           Db         2833NPAEPTSSSPAG                                                                                                                                                                                                                                                                                     | 0 0                                                                                                                              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
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| A;Accession: T06291 A;Accession: T06291 A;Rolecule type: DNA A;Rosidues: 1-760 SEEV. A;Cross-references: EMBL:AL049608 A;Experimental source: cultivar Columbia; BAC clone T9E8 A;Experimental source: cultivar Columbia; BAC clone T9E8 A;Map position: 4 A;Match: T9E8.80 Query Match Best Local Similarity 23.6%; Pred. No. 0.00011; Matches 78; Conservative 26; Mismatches 107; Indels 119; Gaps 13; | OY 28 LVTVAVPATANADPEDAPPVPTTAASPSTAAAPPAPATPANAPPAAANTPNAQPGD 85  398 VVTPLPPRSLPSPPAPITESTPPTLTSPPPSPPPPPPPPPPPPPPPPPPPPPPPPPP | RESULT 14 WMSEHG ULJ6 protein - human herpesvirus 1 (strain 17) C.Species: human herpesvirus 1 C.Species: human herpesvirus 1 C.Species: human herpesvirus 1 C.Species: human herpesvirus 1 C.Species: human herpesvirus 1 C.Species: human herpesvirus 1 C.Species: human herpesvirus 1 C.Species: jalber 2: pair your 2: pair 3: pai |

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GenCore version 5.1.6
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OM protein - protein search, using sw model

July 7, 2004, 18:17:39 ; Search time 10.5 Seconds
(without alignments)
1611.695 Million cell updates/sec Run on:

US-10-720-192-3 1726 1 MHQVDPNLTRRKGRLAALAI.......PAGEVAPTPTTPTPQRTLPA 325 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

|        |       | æ     |        |            | SUMMARIES  |                    |
|--------|-------|-------|--------|------------|------------|--------------------|
| Result |       | Query |        |            |            |                    |
| No.    | Score | Match | Length | DB :       | ΠD         | ptio               |
| rH     | 1726  |       | 325    | -          | APA MYCTU  | OS0906 mycobacteri |
| 7      |       | σ.    | 325    | Н          | APA_MYCBO  |                    |
| m      | 985   | ٠     | 381    | ٦          | APA_MYCAV  |                    |
| 4      | 980   | 56.8  | 287    | ۲          | APA_MYCLE  |                    |
| S      | N     | ٠     | 555    | Н          | GP1 CHLRE  | _                  |
| ø      | 217.5 | ٠     | 817    | Н          | VRPI YEAST |                    |
| 7      | 13    | •     | 3164   | Н          | TEGU_HSV11 |                    |
| œ      | 210   | •     | 1083   | Н          | T2D3 HUMAN | homo s             |
| σ      | N     | 12.0  | 439    | Н          | XP2 XENLA  |                    |
| 10     | 205.5 | ij    | 802    | Н          | ENAH MOUSE | mus musc           |
| 11     | N     | ä     | 3421   | Н          | TEGU_HSVEB |                    |
| 12     | 197.5 |       | 865    | Н          | CPN DROME  | drosop             |
| 13     | 197   | ä     | 283    | -          | EXTN SORBI |                    |
| 14     | 193   | ä     | 620    | Н          | EXIN_TOBAC | nicotian           |
| 15     | 192.5 | ä     | 1198   | Н          | HCN4_RAT   |                    |
| 16     | _     | ä     | 1386   | Н          | ZAP3 MOUSE | mus mus            |
| 17     | 189.5 | •     | 267    | Н          | EXIN MAIZE | zea                |
| 18     | 189   | ä     | 1794   | Н          | YDC9_SCHPO | schi               |
| 19     | Н     | Η.    | 2167   | Н          | SHK1_RAT   |                    |
| 20     | 188.5 | ö     | 2715   | н          | MLL4 HUMAN |                    |
| 21     | П     | ö     | 669    | н          | VGLG_HSV2H | herpe              |
| 22     | 186.5 | ö     | 5179   | Н          | MUC2_HUMAN | Q02817 homo sapien |
| 53     | 186   | ö     | 331    | Н          | PRP1_HUMAN | homod              |
| 24     | Н     | Ö     | 1033   | <b>~</b> 1 | IF2_STRCO  | strep              |
| 52     | 82    | 10.7  | 1300   | ۳I         | SAL3 HUMAN |                    |
| 9      | 4     |       | 633    |            | ZICS_HUMAN | homo               |
| 27     | 84    | ö     | 1046   |            | IF2_STRAW  | strep              |
| 79     | 184   | ö     | 1271   |            | RBMG HUMAN |                    |
| 53     | 183   | 。     | 347    |            | CSP_PLABA  | plasm              |
| 30     | Н     | 。     | 261    | 7          | PRP2 MOUSE | ~1                 |
| 35     | 80    | 。     | 53     | н          | APG_ARATH  | arab               |
| 32     | 180.5 |       | 2716   | Н          | OSA_DROME  | drosophila         |
| 33     | 79    |       | 14     | Н          | BATZ_HUMAN | P48634 homo sapien |
|        |       |       |        |            |            |                    |

| P06915 plasmodium<br>Ogndeo homo sanien | 043426 homo sapien | Q9y566 homo sapien       | P46379 homo sapien | P42768 homo sapien<br>015637 homo sapien | 09y4h2 homo sapien<br>09y618 h nuclear r |
|-----------------------------------------|--------------------|--------------------------|--------------------|------------------------------------------|------------------------------------------|
| CSP_PLABE<br>CM32_HUMAN                 | SYJ1_HUMAN         | SHK1_HUMAN<br>TRX2_MOUSE | BAT3 HUMAN         | WASP_HUMAN<br>SF01_HUMAN                 | IRS2_HUMAN<br>NCR2_HUMAN                 |
| <b>근</b> 근                              |                    |                          |                    | НН                                       | нн                                       |
| 339<br>245                              | 1575               | 2161                     | 1132               | 502<br>639                               | 1324                                     |
| 10.4                                    | 10.3               | 10.3                     | 10.2               | 10.1                                     | 10.1                                     |
| 179                                     | 177.5              | 177                      | 176.5              | 174.5                                    | 174.5<br>174.5                           |
| 3.4<br>3.5                              | 36<br>37           | 89 65<br>67 67           | 4<br>4<br>1        | 4<br>4<br>3<br>8                         | 4 4<br>5                                 |

# ALIGNMENTS

Bacteriol. 184:5479-5490(2002)

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                                                                                                                                                                                  Dobos K.M., Swiderek K., Khoo K.-H., Brennan P.J., Belisle J.T.; "Evidence for glycosylation sites on the 45-kilodalton glycoprotein of Mycobacterium tuberculosis."; Infect. Immun. 63:2846-2853(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BIOTECHNOLOGY: Major immunodominant antigen that has potential as a vaccine against tuberculosis. APA-ELISA could be used in
                                                                                                                                                                                                                                                                                                                                                                      J. Bacteriol. 178:2499-2000-1018 [8]
[8]
SECURINCE OF 40-49, AND CHARACTERIZATION OF CARBOHYDRATE-LINKAGE SITES
BY MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECUENCE OF 40-57, AND CHARACTERIZATION OF CARBOHYDRATE-LINKAGE SITES BY MASS SPECTROMETRY.
STRAIN-H37Rv;
                      PARTIAL SEQUENCE, AND CHARACTERIZATION.
MEDLINE=91099989; PubMed=1898899;
Nagai S., Wiker H.G., Harboe M., Kinomoto M.;
"Isolation and partial characterization of major protein antigens in the culture fluid of Mycobacterium tuberculosis.";
Infect. Immun. 59:372-382(1991).
                                                                                                                                                                                                                                                                                               MEDLINE=96196153; PubMed=8626314;
Dobos K.M., Khoo K.H., Swiderek K.M., Brennan P.J., Belisle J.T.;
"Definition of the full extent of glycosylation of the 45-kilodalton glycoptotein of Mycobacterium tuberculosis.";
J. Bacteriol. 178:2498-2506(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis. MISCELLANEOUS: Changes in the mannosylation pattern of this protein affect its ability to stimulate T-lymphocyte response. CAUTION: Was originally thought to be involved in molybdenum
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MEDLINE-ZONG,
MEDLINE-ZONG,
MEDLINE-ZONG,
Horn C., Namane A., Pescher P., Riviere M., Romain F., Puzo G.,
Barzu C., Marchal G.;
"Decreased capacity of recombinant 45/47-kDa molecules (Apa) of
Mycobacterium tuberculosis to stimulate T lymphocyte responses
related to changes in their mannosylation pattern.";
J. Biol. Chem. 274:32023-32030(1999).
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EMBL; X99258; CAA67645.1; -.
EMBL; AE007044; AA46179.1; -.
EMBL; AE007044; AA46179.1; -.
EMBL; AF07066; D70666.
TIGR; MI1908; -.
TIGR; MI1908; -.
TANDERCULIST; RV1860; -.
Antigen; Glycoprotein; Repeat; Signal; Complete proteome. SIGNAL
40 325 ALANINE AND PROLINE-RICH SEGI
                                                                                                                                                                                                                                                                              PARTIAL SEQUENCE, AND CARBOHYDRATE-LINKAGE SITES.
                                                                                                                                                      PARTIAL SEQUENCE, AND GLYCOSYLATION. MEDLINE=95347792; Pubmed=7622204;
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MEDAINE=22709107; pubMed=12788972;
MEDAINE=22709107; pubMed=12788972;
GarnNer T., Eighmeler K., Camus J.-C., Medina N., Mansoor H.,
GarnNer T., Eighmeler K., Camus J.-C., Monsempe C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrell B.G., Colle S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Alanina and proline-rich secreted protein apa precursor (Fibronectin
attachment protein) (45/47 kDa antigen) (FAP-B).
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                     4 AA APPROXIMATE REPEATS OF [DA] -P-
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                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                          Score 1726; DB 1; Length 325;
Pred. No. 1.5e-80;
; Mismatches 0; Indels 0;
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NCBL_TaxID=1765;
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Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
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P46842; 032905; Q9R5V6;
01-N0V-1995 [Rel. 32, Created)
16-CCT-2001 [Rel. 40, Last sequence update)
28-FEB-2003 [Rel. 41, Last annotation update)
Alanine and proline-rich secreted protein apa precursor (Antigen 43L)
(Fibronectin attachment protein) [FAP-L).
(Fabronectin latrachment protein) [FAP-L).
Mycobacterium laprae.
MEDLINE=97011577; PubMed=8858587; Schorey J.S., Holsti M.A., Ratliff T.L., Allen P.M., Brown E.J.; "Characterization of the fibronectin-attachment protein of Mycobacterium avium reveals a fibronectin-binding motif conserved
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ALANINE AND PROLINE-RICH SECRETED PROTEIN APA.
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                                                                                                                  among mycobacteria.";
Mol. Microbiol. 21:321-329(1996).
-:- SUBCELLULAR LOCATION: Secreted.
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SEQUENCE FROM N.A.
MEDLINE=94086110; PubMed=8262636;
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                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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BY SIMILARITY.
ALANINE AND PROLINE-RICH SECRETED PROTEIN
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3 X 4 AA APPROXIMATE REPEATS OF [DA]-P-
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30-MAX-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alamine and proline rich secreted protein apa precursor (45/47 kDa antigen) (Fibronectin attachment protein) (FAP-A).
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Pred. No. 3e-80;
0; Mismatches 1; Indels (
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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SUBCELLULAR LOCATION: Secreted
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Matches 324; Conservative
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30-MAX-2000 (
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                                                                                                                                                                                                                                                                 "A Mycobacterium leprae gene encoding a fibronectin binding protein is used for efficient invasion of epithelial cells and Schwann cells."; Infect. Immun. 63:2652-2657(1995).
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ALANINE AND PROLINE-RICH SECRETED PROTEIN
                                                                                                                                                               SEQUENCE FROM N.A.
MEDILAB-95310024; PubMed=7790081;
Schorey J.S., Li Q., McCourt D.W., Bong-Mastek M., Clark-Curtiss J.E.
Ratliff T.L., Brown E.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLIRE=21128732; PubMed=11234002;
Cole S.T., Tajlaneiar K., Parkhill J., James K.D., Thomson N.R.,
Mueeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Gaps
Wieles B., van Agterveld M., Janson A., Clark-Curtiss J.B.,
Rinke de Wit T.F., Harboe M., Tholb J.;
"Characterization of a Mycobacterium leprae antigen related to the
secreted Mycobacterium tuberculosis protein MPT32.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 980; DB 1; Length 287; Pred. No. 3.7e-43;
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3 X 4 AA REPEATS OF D-P-N-A.
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Nature 409:1007-1011(2001).
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Leproma, ML2055; -.
Antigen, Repeat; Signal; Complete proteome.
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EMBL, AL583924; CAC3T010.1; -.
EMBL, AL008609; CAA15433.1; -.
                                                                                                         Infect. Immun. 62:252-258(1994).
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287 AA;
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96
241 GVIGSPAANAPDAGPPORWFVVWLGTANNPVDKGAAKALAESIRPLVAPPPAPAPAPA 298
                                                   227 SVVGSPAASTPDVGPSQRWFVVWLGTSNNPVDKGAAKELAESIRSEMAPIPASVSAPA 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Glycosylated polyproline II rods-with-kinks as a structural motif in plant hydroxyproline-rich glycoproteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39 ADPEPAPPVPITAASPPSTAAAPPAAATPV--APPPPAAANTPNAQPGDPNAAPPPADPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PARTIAL PRELIMINARY SEQUENCE FROM N.A. MEDLINE=9101564; Delable 109225; Addit W.S., Apt K.E.; Media W.S., Apt K.E.; Media W.S., Apt K.E.; Media W.S., Apt M.S., Apt M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chiamydomonas reinhardtii.
Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales;
Chlamydomonadaceae, Chlamydomonas.
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49 X 5 AA APPROXIMATE PPSPX REPEATS.
POLY-PRO.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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MEDLINE=21159052; PubMed=11258910;
Ferris P.J., Woessner J.P., Waffenschmidt S., Kilz S., Drees J.,
Goodenough U.W.;
                                                                                                                                                                                                                                                                                                       GPI_CHLRE STANDARD; PRT; 555 AA.

99FPQ6; Q03927;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
Vegetative cell wall protein gpl precursor (Hydroxyproline-rich GPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 555;
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6.8e-06;
ches 69;
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; Pred. No. 6.8e
21; Mismatches
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SEQUENCE 52382 / AB972;

MEDLINE=52382 / AB972;

MEDLINE=52382 / AB972;

MEDLINE=52313267; PubMed=9169871;

A Cohnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W., Benes V., Brueckner M., Coffeau A., Hebling U., Heumann K.,

Benes V., Brueckner M., Goffeau A., Hebling U., Heumann K.,

Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Koetter P.,

Louis B.J., Messenguy F., Mewes H.-W., Miosga T., Moestl D.,

Mueller-Auer S., Nentwich U., Obermaier B., Piranandi E., Pohl T.M.,

Nortecelle D., Purnelle B., Rechmann S., Rieger M., Riake M.,

Scharfe M., Schorrens B., Scholler P., Schwager C., Schwarz S.,

Underwood A.P., Urestarazu L.A., Vandenbol M., Verhassell P.,

Nedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.,

"The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.",

"The matter 387:87-90(1997).

"The PUNCTION: Involved in cytoskeletal organization and cellular

Growth May exert its effects on the cytoskeleton directly, or

indirectly via proline-binding proteins (e.g. profilin) or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                 157 PPVANDTRIVLGRLDQKLYASAEATDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANG 216
                                                                                                                                                  217 VSGSASYYEVKFSDPSKPNGQIWTGVIGSPAANAPDAGPPQRWFVVWLGTANNPVDKGAA
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GermOnline; 142401; -.
SGD; S0004329; VRP1.
GO; GO:0005857; C:actin cortical patch (sensu Saccharomyces); IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Verprolin.

VRP1 OR WDP2 OR END5 OR YLR337W OR L8300.13.

Saccharomyces cerevisiae (Baker's yeast).

Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95058201; PubMed=7968536; Donnelly S.F.H., Pocklington M.J., Pallota D., Orr E.; Donnelly S.F.H., Verprolin, involved in cytoskeletal organization and cellular growth in the yeast Saccharomyces
                                                                                                                                                                                                                                                           277 KALAESIRPLVAPPPAPAPAPAPAPAPAPAPAGEVAPTPT-TPTP 319
                                                                                                                                                                                                                                                                                             302 -----PPTPPSPSPSPSPVPPSPAPVPPSPAPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                             VRP1_YEAST STANDARD; PRT; 817 AA. P37370, 206133; U-CCT-1994 (Rel. 30, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 10-CCT-2003 (Rel. 42, Last annotation update)
263 APPPPSPPPPPPP----RP----PFPA--
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EMBL; U19028; AAB67263.1; -.
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                                                                                                      294 PP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-----PPLPAAMSSASTNSVKATPVPPTLA------PPLPN---TTSVPPNKA 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RPFQNKTKLYPSGKGSSVPLDLTLFT -> HLRWIPVPLIA PVKTLNNGYFLQVDRRCNTSIIRIQINQMLM (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DVGRYTIGGSNSIVGAKSGNERIVIDDSRFKWTNVSQMPKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTSNSPSKNLKQRLFSTGGSTLQHKHNTHTNQPDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASAPPIPGAVPSVAAPPIPNAPLSPAPAVPSIPSSSAPPIPDIPSSAAPPIPIVPSSPAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLPLSGASAPKVPONRPHMPSVRPAHRSHORKSSNISLPSVSAPPLPSASLPTHVSNPPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97 APPPPV-----IAP--NAPOPVRIDNPVGGFSFALPAGWVESDAAHFDYGS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 APPPPPTIGLDSKNIKPTDNAVSPPSSEVPAGGLPFL----AEINARRSERGAVEGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----ALLSKTTGDPPFPGQPPPVAND-----TRIVLGRLDQKLYASAEATDSKAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188 RLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFSDPSKPNGQIWTGVIGSPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31; Mismatches 125; Indels 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24C7522D5B1CA1C8 CRC64;
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
NCB_TaxID=10299;
GO; GO:0003779; F:actin binding; IDA.
GO; GO:0007015; P:actin binding; IDA.
GO; GO:0007015; P:actin filament organization; IPI.
GO; GO:0007121; P:polar budding; IMP.
GO; GO:0006970; P:response to osmotic stress; IMP.
GO; GO:0006970; P:response to osmotic stress; IMP.
InterPro; IPR003124; WH2.
SWARY; SW00246; WH2; 2.
SWARY; SW00246; WH2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.6%; Score 217.5; DB 1; 26.3%; Pred. No. 0.00018;
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A -> R (IN REF. 1).
V -> E (IN REF. 1).
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01-MAR-1989 (Rel. 10, Last seq
01-APR-1993 (Rel. 25, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     817 AA; 82593 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPP----PPTLTTNKP 452
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Best Local Similarity
Matches 99; Conserv
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P10220;
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SEQUENCE FROM N.A.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2742 IPLGPQAAGQASPALPIDPVPPPVATGT---VLPGGENRRPPLTSGPAPTPPRVPVGGPQR 2799
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 REKGRLAALAIAAMASA-----SLVTVAVPATANADPEPAPPVPTTAASPPSTAAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 ------PAPATPVAP-PPPAAANTPNAQPGDPNAAPPPADPNAPPPVIAPNAPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171 DOKLYASABATDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFSD
                                                                                            ij
SEQUENCE FROM N.A.

MEDLINEse8874327, PubMed=2839594;

MCGeoch D.J., Dalrymle M.A., Davison A.J., Dolan A., Frame M.C.,

MCNab D., Perry L.J., Scott J.E., Taylor P.;

MCNab D., Perry L.J. Scott J.E., Taylor P.;

McNab D., Perry L.J. Scott J.E., Taylor P.;

her complete DNA sequence of the long unique region in the genome of the person simplex virus type 1.";

J. Gen. Virol. 69:1531-1574(1968).

-! FUNCTION: Tegument procein.

-! FUNCTION: Tegument procein.

-! FUNCTION: Tegument procein.

-! FUNCTION: Tegument procein.

-! ENLIARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36,

EHV-1 24, EBV BPLF1, HVS-1 64, VZV 22, AND HCMV UL48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , Score 213.5; DB 1; Length 3164; Pred. No. 0.001; 17; Mismatches 117; Indels 119;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; 130085; WMBEH6.
InterPro; IPR006928; Herpes teg N.
InterPro; IPR005210; Herpes_UL36.
Pfam; PF04843; Herpes_teg N; 1.
Pfam; PF03586; Herpes_UL36; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X14112; CAA32311.1; -.
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26.5%;
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Best Local &
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NEUTINE=21638749; PubMed=11780052;

NEDLINE=21638749; PubMed=11780052;

NEDLINE=21638749; PubMed=11780052;

Deloidas P., Matthews L.H., Ashurst J., Babbage A.K., Bagguley C.L., Balley J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Basley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., Buck D., Burrill W.D., Buller A.P., Carder C., Carter N.P., Chapman J.C., Colley V. B., Collier R.E., Connor R.E., Corby N.R., Coulson A., Coville G.J., Deadman R., Dhanh P.D., Dunn M., Blington A.G., Frankland J.A., Fraser A., French L., Garner P., Blington A.G., Frankland J.A., Fraser M.D., Gwilliam R., Hall R.E., Fammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., Andrews J. Hantley J.L., Hath P.D., How J., Howden P.J., Howele E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., Andrews G. M. Miller J.D., McConnachie L.J., McLay K., McMurray A.B., Hulte S.L., McConnachie L.J., McLay K., McMurray A.B., Mille S.L., Matel R.J., Partel R., Milley D., Moore M.J.F., Mullikin J.C., Nickerson T., Anile S.M., Mister D., Patel R., Plumb R.W., Ramesay H., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S., Swann R.M., Sysamore N., Taylor R., Thomas D.W., Thorpe A., Swann R.M., Sysamore N., Taylor R., Thomas D.W., Thorpe A., Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J., Williams D.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Davidson I.;
"The human TFIID components TAF(II)135 and TAF(II)20 and the yeast
SAGA components ADA1 and TAF(II)68 heterodimerize to form histone-like
       MEDIJINE-97336072; PubMed-9192867; Mengus G., May M., Carre L., Chambon P., Davidson I.; Mengus G., May M., Carre L., Chambon P., Davidson I.; "Human TAR(II)135 potentiates transcriptional activation by the AF-2s of the retinoic acid, vitamin D3, and thyroid hormone receptors in mammalian cells."; Genes Dev. 11:1381-1395(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUPTIH, TAF2, TAF5, TRRAP, GCN5L2 AND TAFIO.
MEDLINE-99303588; PubMed-10373431;
Brand M., Yamamoto K., Staub A., Tora L.,
"Identification of TATA-binding protein-free TAFII-containing complex subunits suggests a role in nucleosome acetylation and signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The DNA sequence and comparative analysis of human chromosome 20.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 105-1083 FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-97096442; PubMed-8942982;
Tanese N., Saluja D., Vassallo M.F., Chen J.-L., Admon A.;
"Molecular cloning an analysis of two subunits of the human TFIID complex: htarili30 and htarili00.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y.-G., Werten S., Romier C., Carre L., Poch O., Moras D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDENTIFICATION IN THE TFTC-HAT COMPLEX WITH TAF5L; TAF6L; TADA3L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        K-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 870-918 IN COMPLEX WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  roc. Natl. Acad. Sci. U.S.A. 93:13611-13616(1996).
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SUBCELLULAR LOCATION: Nuclear

T2D3 HUMAN STANDARD; PRT; 1083 AA.

000268; Q99721; Q9BR40; Q9BK42;

15-JUL-1998 (Rel. 36, Created)

15-JUL-1998 (Rel. 34, Last annotation update)

15-MAR-2004 (Rel. 43, Last annotation update)

15-MAR-2007 (Rel. 43, Last annotation update)

17ARR-2007 (Rel. 43, Last annotation update)

17ARI-135 (TAFII-130) (TAFII-130)

17AF4 OR TAFA4 OR TAFZCI OR TAFZC OR TAFIII35 OR TAFIII30.

Homo sapiens (Human).

Y RXX

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. NCBL\_TaxID=9606; [1]

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TISSUE=Skin;
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                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 AAN--TPNAQPGDPNAAPPPADPNAPPPVIAPNAPQP-VRIDNPVGGFSFALPAGWV-- 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 ----ESDAAHFDYG----SALLSKTTGDPPFPGQPPPVANDTRIVLGRLDQKLYASAEAT 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 DSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFSDPSKP----NGQ 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 LAALAIAAMASASLVTVAVPATANADPEPAPPVPTTAASPPSTAAAPPAPATPVAPPPPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92;
                                                                                                                                                                                                   MIM, 601796; -...
GO; GO: 0005569; C: transcription factor TFIID complex; TAS.
GO; GO: 00016511; F: general RNA polymerase II transcription fac.
GO; GO: 00055115; F: protein binding; TAS.
GO; GO: 0003713; F: transcription co-activator activity; TAS.
InterPro; IPRO7900; TAF4.
InterPro; IPRO3989; TAFF, IAF, IAF.
                                                                                                                                                                                                                                                                                                       000 regulation; Nuclear protein; 3D-structure.
590 682 TAFH/NHR1.
52 42 POLY-HIS.
52 57 POLY-GLY.
142 148 POLY-GLY.
142 148 POLY-ALA.
56 37 POLY-ALA.
56 83 POLY-ALA.
680 683 POLY-PRO.
680 883 POLY-PRO.
70LY-ALA.
680 883 POLY-PRO.
828 831 POLY-ALA.
105 117 PGPPSPRRPLVPA -> GRGLLQQRGGRES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.2%; Score 210; DB 1; Length 1083; 27.8%; Pred. No. 0.00056; tive 20; Mismatches 140; Indels 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A - S (IN REF. 2).

G -> GPG (IN REF. 2).

MISSING (IN REF. 3).

P -> L (IN REF. 3).

Ww, A6453827572A0752 CRC64;
SIMILARITY: BELONGS TO THE TAF2C FAMILY. SIMILARITY: Contains 1 TAFH/NHR1 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             449 LPPGMVLVRSENGQLLMIPQ-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                              (IN REF.
                                                                                                                        EMBL; Y11354; CAA72189.1; -.
EMBL; AL137077; CAC36006.1; -.
EMBL; AL109911; CAC22312.2; -.
                                                                                                                                                          EMBL; U75308; AAC50901.1; -. PDB; LH30; 26-SEP-02. TRANSFAC; T02328; -. Genew; HGNC:11537; TAF4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109943
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293
1083 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
tes 97; Conserv
                                                                                                                                                                                                                                                                                                            Transcription
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YER YERLA STANDARD; PRT, 419 AA.

De 17437, 008947.

De 17487, 008947.

De 174887.

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  129
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                                                                                                                                                                                                                             ESDAAHFDYGSALLSKTTGDPPFP----GQPPPVANDTRIVLGRLDQKLYASAEATDSKA 185
                                                                                                                                                                                                                                                 BAPAP-----APAEGEAPAPAPAEGEAPAPAP-------AEGEAPAPAP 201
                                                                                                                                                                                                                                                                                        AB-----GEAPAPAPARGEAPAPARGEAPAPAEGEAPAPARGGEAPAPARGE-----A 248
                                                                                                                                                                                                                                                                                                            PA----ANAPDAGPPORMFVVWLGTANNPV---DKGAAKALAESIRPLVAPPPAAPAP 297
                                                                                                                                                                  PAPAPAEGEAPAPAEGGAPAPAPAEGAEPAPADGGAPAPAFGGAPAPAEGGAPAPA 104
                                                                                                                                                                                                                                                                                                                                82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDILINE=97015079; PubMed=8861907;
Gertler F.B., Niebuhr K., Reinhard M., Wehland J., Soriano P.;
"Mena, a relative of VASP and Drosophila Enabled, is implicated in the
control of microfilament dynamics.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS 2; 3; 4 AND 5), FUNCTION, AND SUBCELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                          ENAH WOUSE STANDARD; PRT; 802 AA.

Q03173; P70430; P70431; P70433;

Q01-071-1996 (Rel. 34. Created)

10-0CT-2003 (Rel. 42. Last sequence update)

10-0CT-2003 (Rel. 42. Last annotation update)

Enabled protein homolog (NPC derived proline-rich protein 1) (NDPP-1).
                                                                                                                                            PATANADPE-PAP-----PVPTTAASP-PSTAAAP-PAPATPVAP-PPPAAANTPNAQ
                                                                                                                                                                                       PGDPNA------APPPADPNAPPPVIAPNAPQPVRIDN----PVGGFSFALPAGWV
                                                                                                                                                                                                 AARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFSDPSKPNGQIWTGVIGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1).
TISSUBBRAIN:
MEDILINE=904192; PubMed=1420303;
Sazuka T., Tomooka Y., Kathju S., Ikawa Y., Noda M., Kumar S.;
Sazuka T., Tomooka Y., Rathju S., Ikawa Y., Noda M., Kumar S.;
"Identification of a developmentally regulated gene in the mouse
"Identification of a developmentally regulated gene in the mouse
central nervous system which encodes a novel proline rich protein.";
Biophys. Acta 1132:240-248(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                          80;
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FUNCTION, AND SUBUNIT.
MEDLINE=99166867; PubMed=10069337;
Lanier L.M., Gates M.A., Witke W., Menzies A.S., Wehman A.M.,
                                                                                                     ; Score 207; DB 1; Length 43; Pred. No. 0.00035; 21; Mismatches 132; Indels
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
Missing (in isoform 2).
//TIdevSP 004652.
H -> S (IN REF. 2).
C -> W (IN REF. 2).
W; 38C4A4B57CBAE778 CRC64;
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| AEGEAPAPAPAEGGAPSPAEGGAPAAPA 330
                                                                                                                                                                                                                                                                                                                                                       AE-PAPAPAGEVAPTPTTPTPQRTLPA 325
                                                                                 41173 MW;
                                                                                                      12.0%;
29.2%;
                                                                                                                           Conservative
  388
424
423
4423
343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                 439 AA;
                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Brain;
                                                                                                                           96;
                    DISULPID
DISULPID
VARSPLIC
                                                             CONFLICT
CONFLICT
SEQUENCE
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  DISULFID
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way willied and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Missing (in isoform 4).
/FTIGE-VSP 007257.
CIFC -> VFYL (in isoform 4).
/FTIGE-VSP 007258.
Missing (in isoform 2 and isoform 3).
/FTIGE-VSP 007259.
Macklis J.D., Kwiatkowski D., Soriano P., Gertler F.B.;
"Mena is required for neurulation and commissure formation.";
Neuron 22:131-325(1999).
-!- FUNCTION: May be involved in microfilament assembly and cell
motility. Induces the formation of F-actin rich outgrowths in
fibroblasts. Required for neurulation and commissure formation.
-!- SUBGNIT: Binds profilin.
-!- SUBGRILUIAR LOCATION: Localized to focal adhesions and, to a
lesser extent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=3; Synonyms=Mena+;
IsoId=Q03173-4; Sequence=VSP_007259;
Name=4; Synonyms=Mena++;
IsoId=Q03173-5; Sequence=VSP_007257, VSP_007258;
-:- TISSUE SPECIFICITY: In the heart and testis and less so in the lung; skeletal muscle, kidney, pancreas and brain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPQHFLLPQDPLHHLHCHPLVLLLHPLHPLFLI
HLLPLPSPHLEFSLDPRQKTIAFNWTCSCNCGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neurogenesis; Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=2; Synonyms=Mena;
IsoId=203173-3; Sequence=VSP_007259, VSP_007260;
                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=Q03173-2; Sequence=VSP_007255, VSP_007256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO, GO:0005925; C:focal adhesion, IDA.
GO; GO:0005522; F:profilin binding; IDA.
GO; GO:0017124; F:SH3-domain binding; IDA.
GO; GO:0017015; P:actin filament organization; IDA.
GO; GO:0007015; P:actin filament organization; IDA.
GO; GO:0007411; P:axon guidance; IMP.
GO; GO:0006528; P:cell motility; IDA.
GO; GO:001679; P:eurulation; IDA.
InterPro; IPR001960; WH1.
SWART; SM00461; WH1.
Developmental protein; Neurogenesis; Alternative splic
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Missing (in isoform 2)
                                                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=5;
Name=5; Synonyms=Mena+++;
IsoId=Q03173-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     007255
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EMBL; U72521; AAC52864.1;
EMBL; U72523; AAC52865.1;
EMBL; U72523; AAC52866.1;
PIR; S27200; S27200.
MGD; MGI:108360; Enah.
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                                                                                                                                                                                                                                                                              -!- ALTERNATIVE PRODUCTS:
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                                                                   11;
                                                                                                                  343 VPRPLNKNSRPSSPVNTPSSQPPAAKSCAWPTSNFSPLPPSPPIMISSPPGKATGPRPVL 402
                                                                                                                                                    PAAANTPNAQ----PGDPNAA-----PPPADPNAPPPPVIAPNAPQPVRIDNPVG 118
                                                                                                                                                                               454
                                                                                                                                                                                                                                   178 AEATDSKAAARLGSDMGEFYMPYPGTRI-----NQETVSLDANGVSGSAS---YYEVKF 228
                                                                                                                                                                                                                                                                                                                     SDPSKPNGQIWTGVIGSPAANAPDAGPPQRWFVVWLGTANNPVDKGAAKALAESIRPLVA 288
                                                                                                                                                                                                                                                                                                                                      GFSFALPAGWVESDAAHFDYGSALLSKTTGDPPFPGOP-PPVANDTRIVLGRLDOKLYAS 177
                                                                                               72
                                                                                                                                                                                                                                                                                         -----LSHCGSQASPPEGTPLASTPSSKPSVLPSPSAGAPASAETPLNPELGD
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDINE=92295566; PubMed=1318606;

Helford E.A.R., Watson M.S., McBride K., Davison A.J.;

"The DNA sequence of equine herpesvirus-1.";

Virology 189:304-316(1992).

-!- FUNCTION: TEQUENT PROTECHIN.

-!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36,

EHV-1 24, EBV BPLF1, HVS-1 64, VZV 22, AND HCMV UL48.
                                                                   Indels 123;
                                                                                                                                                                            PVCVSSPVPQMPPSPTAPNGSLDSVTYPVSPPTSGPAAPPPPPPPPPPPPPPPPPPPP
                                         DB 1; Length 802;
                                                                                             33 VPATANADPEPAPPVPTTAASPPSTAAA------PPAPATPVAPPP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 3421;
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PIR; G36797; WZBEB6.
InterPor, IPR006928; Herpes teg N.
InterPror; IPR005210; Herpes UL36.
Pfam; PF04843; Herpes Leg N, 1.
Pfam; PF03586; Herpes UL36; 1.
Pfam; PF03586; Herpes UL36; 1.
/FTId=VSP_007260.
: 592BB975EE20F77F CRC64;
                                                                                                                                                                                                                                                                                                                                                                           ---PPPAPAPAABPAPAPAGEVAPTPTTPTPQRTLPA 325
                                                                                                                                                                                                                                                                                                                                                                                                    PPPPPPLPSTGPPPPPPPLPNOAPPPPPPPPP 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.
Equine herpesvirus type 1 (strain Ab4p) (EHV-1),
Viruses, dsDNA viruses, no RNA stage; Herpesviridae,
Alphaherpesvirinae; Varicellovirus.
                                       11.9%; Score 205.5; DB 1; 22.9%; Pred. No. 0.00072; ive 27; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           203; DB 1;
No. 0.0036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 24, Last sequence update)
(Rel. 25, Last annotation update)
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Pred.
             85844 MW;
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23.9%;
                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Large tegument protein.
             802 AA;
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Best Local Similarity
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01-DEC-1992 (
01-APR-1993 (
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              SEQUENCE
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  15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2784 QSTKEPPK-------PAVETPAAPAK-----SAAAPAAPAAPAKSAAPAAPA 2823
                                                                                                                          108
                                         09
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MEDLINE=93165729; PubMed=8094559;
Martin J.H., Benzer S., Rudnicka M., Miller C.A.;
"Calphotin: a Drosophila photoreceptor cell calcium-binding protein.";
Proc. Natl. Acad. Sci. U.S.A. 90:1531-1535(1993).
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                                                                                 PTLPPKAAPLPPSDASAIMSGKPVFKYTPGNKSAVPPSVPAPPTLPPAPPLPQSTSKAAS
                                                                                                                                                                                                                                                                                                                                                                       167 LGRLDQKLYASAEATDSKAAARLGSDMGEF-YMPYPGTRINQETVSLDANGVSGSASYYE
                                         PNLTRRKGRLAALAIAAMASASLVTVAVPATANADPEPAPPVPTTAASPP----STAAA
                                                                                                                        61 PPAPATPVAPPPPAAANTPNAQPGDPNAAPPPADPNAP------PPPVIAPNAP
                                                                                                                                                                2565 GPPPTLPPAPPLP--QSTSKAASG-----PPPTLPPAPPLPQSTSKAASGPPPTLPPAPP
                                                                                                                                                                                                         ---SFALPAGWVESDAA---
                                                                                                                                                                                                                                               2618 LPQSTSKAASGATQSDSGKTLTLDVPKTQSKDKVVPVPPTDKPSTTTPAALKQSDASKPP
                                                                                                                                                                                                                                                                                          ----FPG-OPP----PVANDTRIV
                                                                                                                                                                                                                                                                                                                                                                                                                 -----QPVRKSLPSQVRGGRPYIRPSLGPFKFTGPPG-----YTIPVHGLPPSDSNVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                        226 VKFSDPSKPNGQIWTGVIGSPAANAPDAGPPQRWFVVWLGTANNPVDKGAAKALAESIRP
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-93165730; PubMed-8434015;
Ballinger D.G., Xue N., Harshman K.D.;
"A Drosophila photoreceptor cell-specific protein, calphotin, binds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          calcium and contains a leucine zipper.";
Proc. Natl. Acad. Sci. U.S.A. 90:1536-1540(1993).
-!- FUNCTION: Might function as a calcium-sequestering "sponge" to regulate the amount of free cytoplasmic calcium. It binds 0.3 m of Ca(2+) per mole of protein.
-!- SUBUNIT: Homodimer (Probable).
Indels 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEVELOPMENTAL STAGE: Expressed early in photoreceptor cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Cytoplasmic; hypodense compartment. IISSUB SPECIFICITY: Some and axons of photoreceptor cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CENTOR CAP.

Drosophila melanogaster (Fruit fly).

Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,

Neoptera, Budopterygota, Diptera, Brachycera, Muscomorpha,

Ephydroidea, Drosophilidae, Drosophila.

NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L-VAPPPAPAPAPAPAPAPAGEVAPTPTTPTPQRTLPA 325
                                                                                                                                                                                                         QPVRIDNPVGGF------
31; Mismatches 152;
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(Rel. 27, Last sequence update)
(Rel. 42, Last annotation update)
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  Conservative
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01-OCT-1993
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  96;
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P13983;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                400 PSA-VAETPVDLAPPVLPPVAAEPVPAVVAEETPETPAPASAPVTIAALDIPEVAPVIAA 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 DSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFSDPSKPNGQIWTG 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            502 VLSEAAIETPVA-----PPVEVTTEVAVAD-----VAPPEAAADLIIEPV 541
                                                                                                                                                                                                                                                                                                                                                             290 ATLITAPETPALAPVVAESQVAANTVVATP--PTPAPEP-ETIAPPVVAETPEVASVAVA 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSALLSKTTGD-----PPFPGQPPP--VANDT-----RIVLGRLDQKLYASAEAT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   459 PSDAPAEAPSAAAPIVSTPPTTASVPETTAPPA-------AVPTEP---IDVS 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 VIGSPAANAPDAGPPORWFVVWLGTANNPVDKGAAKALAESIRPLVAPPPAPAPAPAEPA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                           347 ETTPPVVPPVAAESIPAPVVATTPV-----PATLAVTDPDVTASAVPELPPVIAPSPV 399
                                                                                                                                                                                                                                                                                                                                                                                         ----APATPVAPPPPA----AANTPNAQPGDPNAAPPPADPNAPP-----
                                                                                                                                                                                                                                                                                                                                              15 LAALAIAAMASASLVTVAVPAT----ANADP--EPAPPVPTTAASPPSTAAAPP---
                                                                                                                                                                                                                                                                                                                        30; Mismatches 127; Indels 133; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sorghum bicolor (Sorghum) (Sorghum vulgare).
Shikaryora, Viridiplantae; Streptophyta; Babryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicodéae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                  DB 1; Length 865;
                                                                                                                                                                                                                                                     -> L (IN REF. 2).
-> E (IN REF. 2).
2110417E0B0E7CFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                       100 ----PPVIAPNAPQPVRIDNPVGGFSFALPAGWVESD----
                                                                                                                                       5
                                                                                                                                     A -> AVAPAVVA (IN REF. 2)
I -> T (IN REF. 2)
I -> V (IN REF. 2)
T -> A (IN REF. 2)
P -> PP (IN REF. 2)
VQ -> AP (IN REF. 2)
I -> V (IN REF. 2)
S -> T (IN REF. 2)
A -> E (IN REF. 2)
A -> E (IN REF. 2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-WAR-1992 (Rel. 21, Last sequence update) 30-WAY-2000 (Rel. 39, Last annotation update) Extensin precursor (Proline-rich glycoprotein)
                                                                                                                                                                                                                                                                                                 Score 197.5; DB Pred. No. 0.002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    283 AA
                                                                                                      FlyBase; FBgn0010218; Cpn.
GO; GO:0005509; F:calcium ion binding; IDA
Calcium-binding.
36 A -> AVAPAVVA
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84781 MW; 2
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(Rel. 21, Last seq
(Rel. 39, Last ann
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26.6%;
                                                          EMBL; L02111; AAA28405.1; -. EMBL; L05080; AAA28420.1; -. PIR; A47282; A47283.
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01-MAR-1992
30-MAY-2000
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CONFLICT
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Best Local 8
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DT 30-MAI

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 152
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                                                                                                             Plant Mol. Biol. 16:365-367(1991).
-i- FUNCTION: Structural component in primary cell wall.
-i- PTM: EXTENSINS CONTAIN A CHARACTERISTIC REPRAT OF THE PENTAPEPTIDE SER-PRO(4). THE PROLINE RESIDUE IS HYDROXYLATED AND THEN GLYCOSYLATED.
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnollophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales, Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93 ADPNAPPPVIAPNAPQPVRIDNPVGGFSFALPAGWVESDAAHFDYGSALLSKTTGDPPF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Extensin precursor (Cell wall hydroxyproline-rich glycoprotein)
                                 Raz R., Cretin C., Puigdomenech P., Martinez-Izquierdo J.A.; "The sequence of a hydroxyproline-rich glycoprotein gene from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; S1388; S1338;
Interpro; IPR003882; Pistil_extensin.
PRINTS; PR01218; PSTLEXTENSIN.
Repeat; Cell wall; Glycoprotein; Signal; Structural protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTENSIN.
8D7FCD0DA8ED2D90 CRC64;
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MEDLINE=91370882; PubMed=1893107; Par P Cretin C. Puiddomenech P
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283 EXT
29593 MW; 8
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STRAIN=cv. Xanthi; TISSUE=Leaf;
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01-JAN-1990 (Rel. 13, Last seq
16-OCT-2001 (Rel. 40, Last ann
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283 AA;
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----YSPP- 458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----PPPA 478
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                                                                                                                                                                                                                                                                                                      main root.
SUBCELLULAR LOCATION: Extracellular matrix.
PTM: EXTENSINS CONTAIN A CHARACTERISTIC REPEAT OF THE PENTAPEPTIDE SER-PRO(4). THE PROLINE RESIDUE IS HYDROXYLATED AND THEN GLYCOSYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTENSIN.
H-A-P-P.
H-A-P-P.
2 X 7 AA TANDEM REPEATS OF T-H-R-H-A-P-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 TVAVPATANA-DPEP----APPVPTTAASPPSTAAAPPAPA-----TPV-APPPPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75 AANTPNAQPGDPNAAPPPADP-NAPPPPVIAP-----NAPQPVRIDNPVGGFS
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MEDLINE-90128263; PubMed-2612909; Keller B., Lamb C.J.; Elamb C.J.; Lamb C.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONTAINS THE SER-PRO(4) REPEATS. 3 X APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS, PR00211; GLUTELIN.
Repeat, Cell wall; Glycoprotein, Signal; Structural protein,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ā
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IPR000480; Glutelin.
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Matches 83; Conserv
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InterPro; Il
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ID HCN4_RAT

AC Q9JKA7; QS

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09UKĀ7: Q9QZW4; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update)

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"Werture Tailoland Stokul,"

"Hyperpolarization-activated ion channel with very slow activation and inactivation exhibiting weak selectivity for activation and inactivation exhibiting weak selectivity for potassium over sodium ions. May contribute to the native pacemaker currents in heart (If) and in neurons (Ih). Activated by CAMP. May mediate responses to sour stimuli.

"SUBMIT: The potassium channel is probably composed of a homo- or heterotetrameric complex of pore-forming subunits.

"ISSUB SPECIFICITY: Highly expressed in pyramidal and granule layer of the hippocampus, in thatamus anterior nucleus, in the supraoptic nucleus in hypothalamus, in cerebellum, and in trapezoid nuclei and superior olivary complex in the auditory system. Detected in a subset of elongated cells in taste buds.

"Issubmantant a segment 34 is probably the voltage sensor and is characterized by a series of positively charged amino acids at every third position."

"Hand Defended in a series of positively charged amino acids at every third position."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions and and a sits content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tong as its content is in no way noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION, AND TISSUE SPECIFICITY.
MEDLINE=21530492; PubMed=11675786;
Stevens D.R., Seifert R., Bufe B., Mueller F., Kremmer E., Gauss R.,
Meyerhof W., Kupp U.B., Lindemann B.,
"Hyperpolarization-activated channels HCN1 and HCN4 mediate responses
                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
лэ-гдж-2004 (Rel. 43, Last annotation update)
Potassium/sodium hyperpolarization-activated cyclic nucleotide-gated
channel 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shi W., Wymore R., Yu H., Wu J., Wymore R.T., Pan Z., Robinson R.B., Dixon J.E., McKinnon D., Cohen I.S., "Distribution and prevalence of hyperpolarization-activated cation channel (HCN) mRNA expression in cardiac tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Monteggia L.M., Eisch A.J., Tang M.D., Kaczmarek L.K., Nestler E.J.; "Cloning and localization of the hyperpolarization-activated cyclic nucleotide-gated channel family in rat brain."; Brain Res. Mol. Brain Res. 81:129-139(2000).
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PROSITE; PS00888; CNMP BINDING 1; 1.
PROSITE; PS00889; CNMP BINDING 2; FALSE NEG.
PROSITE; PS50082; CNMP BINDING 3; 1.
Transport; Ion transport; Ionic channel; Voltage-gated channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (sor send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-Sprague-Dawley, TISSUE-Brain,
MEDLINE-20457301, PubMed-11000485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro: IPR000595; cNNP_binding.
InterPro: IPR005811; Ion trans.
InterPro: IPR005820; M+channel_nlg.
Pfam; PP00027; cNNP_binding; 1.
Pfam; PP00520; ion_trans; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99459217; PubMed=10400919;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 262-428 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to sour stimuli.";
Nature 413:631-635(2001)
                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Heart;
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| otassium; Potassium transport; Sodium transport; Transmembrane; Glycoprotein; Sodium channel. GEGMENT SI (POTENTIAL). SEGMENT SI (POTENTIAL). AU CYTOPLASNIC (POTENTIAL). CYTOPLASNIC (POTENTIAL). SEGMENT SI (POTENTIAL). SEGMENT SI (POTENTIAL). CYTOPLASNIC (POTENTIAL). SEGMENT SI (POTENTIAL). SEGMENT SI (POTENTIAL). SEGMENT SI (POTENTIAL). SEGMENT SI (POTENTIAL). SEGMENT SI (POTENTIAL). SEGMENT SI (POTENTIAL). SEGMENT SI (POTENTIAL). SEGMENT SI (POTENTIAL). SEGMENT SI (POTENTIAL). SEGMENT SI (POTENTIAL). CYTOPLASNIC (POTENTIAL). SEGMENT SI (POTENTIAL). CAMP.  INVOLVED IN SUBUNIT ASSEMBLY (BY SIMILARITY). CAMP.  TO VIN REF. 2).  128760 MW; 6B92B8F9452F760F CRC64; | core 192.5; DB 1; Length 1198;  mismatches 124; Indels 153; Gaps                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | -PLSLFGARAASSGGPPLTAAPQREPGARSEPVRSKLPS 1196 |
| T GOWWWWAAANUG COAA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | imilarity 23.8%; Pr Conservative 37;  RRKGRLAALAIAANASASLVT-                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 11d                                          |
| channe<br>1<br>1<br>267<br>294<br>315<br>315<br>316<br>316<br>465<br>465<br>495<br>518<br>518<br>518<br>665<br>67<br>67<br>67<br>64<br>64<br>64<br>64<br>64<br>64<br>64<br>64<br>64<br>64<br>64<br>64<br>64                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Similarity 8; Conserva 8; Conserva 1; Cons | р                                            |
| Potassium<br>CAMP; CAME<br>DOMAIN<br>TRANSMEM<br>TRANSMEM<br>TRANSMEM<br>TRANSMEM<br>TRANSMEM<br>TRANSMEM<br>TRANSMEM<br>TRANSMEM<br>TRANSMEM<br>TRANSMEM<br>TRANSMEM<br>TRANSMEM<br>TRANSMEM<br>ODMAIN<br>DOMAIN<br>DOMAIN<br>DOMAIN<br>CARBOHYD<br>CONFLICT<br>SEQUENCE                                                                                                                                                                                                                                                                                                                                                                                                                    | ωœ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 1158                                         |
| XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 8                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Q<br>Q                                       |

Search completed: July 7, 2004, 18:21:52 Job time : 11.5 secs

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GenCore version 5.1.6
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                  Copyright
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- protein search, using sw model July OM protein Run on:

7, 2004, 18:18:15; Search time 36.5 Seconds (without alignments) 2809.409 Million cell updates/sec

US-10-720-192-3 1726 1 MHQVDPNLTRRKGRLAALAI.......PAGEVAPTPTTPTPQRTLPA 325 score! Title: Perfect sc Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1017041 Total number of hits satisfying chosen parameters: 1017041 seqs, 315518202 residues Searched:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL\_25:\*
1: sp\_archea:\*
2: sp\_bacteria:\*
3: sp\_bacteria:\*
4: sp\_human:\*
5: sp\_invertebrate:\*
5: sp\_mammal:\*
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5: sp\_mammal:\*
5: sp\_mammal:\*
5: sp\_nto:\*
sp\_plant:\*
sp\_rodent:\*
sp\_vinus:\*
sp\_vortebrate:\*
sp\_unclassified:\*
sp\_roirus:\*
sp\_bacteriap:\*
sp\_archeap:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Description                   | Q9r640 mycobacteri | Q9f4h9 mycobacteri | Q8vs65 mycobacteri | Q65553 bovine herp | Q9ask4 oryza sativ | Q7t5d9 simian herp | Q95jd0 sus scrofa | Q95jdl sus scrofa | Q89x06 bradyrhizob | Q7t591 simian herp | Q8w5k6 oryza sativ | Q7xh56 oryza sativ | Q41805 zea mays (m | Q8mxu8 caenorhabdi | Q82du7 streptomyce | Q41645 volvox cart |
|-------------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| OI.                           | Q9R640             | Q9F4H9             | Q8VS65             | 065553             | Q9ASK4             | Q7T5D9             | Q95JD0            | Q95JD1            | 90X68Q             | Q7T591             | QBW5K6             | Q7XH56             | Q41805             | QBMXU8             | Q82DU7             | Q41645             |
| DB                            | 2                  | 7                  | N                  | 12                 | 10                 | 12                 | 9                 | 9                 | 16                 | 12                 | 70                 | 10                 | 10                 | Ŋ                  | 16                 | 10                 |
| %<br>Query<br>Match Length DB | 286                | 368                | 194                | 3247               | 698                | 3288               | 511               | 566               | 745                | 3326               | 1269               | 1269               | 1188               | 668                | 584                | 464                |
| %<br>Query<br>Match           | 89.2               | 61.0               | 32.9               |                    | 14,4               |                    | . *               |                   |                    | 13.9               | 13.8               | 13.8               | 13.8               | 13.4               | 13.4               | 13.2               |
| Score                         | 1539               | 1053.5             | 568                | 256                | 248.5              | 248                | 244               | 244               | 241.5              | 240.5              | 238                | 238                | 237.5              | 231                | 230.5              | 228.5              |
| Result<br>No.                 |                    | 7                  | m                  | 4                  | ហ                  | 9                  | 7                 | 80                | σ                  | 10                 | 11                 | 12                 | 13                 | 14                 | 15                 | 16                 |

|                                                                                                                                                                                           | Q90yb5 gallus gall Q23635 caenorhabdi Q70818 synechococ Q9xib6 arabidopsis Q07229 saccharcmyc Q94847 volvox cart Q95pm0 zea mays (m Q8j065 yarrowia li Q84510 oryza sativ Q94085 arabidopsis P89459 herpes simp Q9107 acanthamoeb Q912n5 streptomyce Q96q04 homo sapien Q39763 gossypium b Q98f98 rhizobium l                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
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| 4 OBNAA1<br>116 QBVKN7<br>116 QBVKN7<br>116 QBFM53<br>5 Q9VZC2<br>6 Q95CQ9<br>110 Q94JZ6<br>6 Q95CQ9<br>110 Q90LV48<br>12 Q90LV48<br>12 Q90LV48<br>110 Q9SEM1<br>110 Q9SEM1<br>110 Q9SEM1 | 13 Q90YB5<br>5 Q23635<br>16 Q23635<br>10 Q9XIB6<br>10 Q9XIB6<br>10 Q95PM0<br>3 Q010E5<br>10 Q84ZL0<br>10 Q84ZL0<br>10 Q84ZL0<br>11 Q84459<br>5 Q92107<br>4 Q96Q04<br>11 Q39763<br>16 Q98F98                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| W W W W W W W W W W W W W W W W W W W                                                                                                                                                     | 784<br>801<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>1001<br>10                                                                                                                                                                                                                                                                                                                                                      |
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| 227.5<br>226.5<br>226.5<br>225.5<br>225.5<br>224.5<br>224.5<br>223.5<br>223.5<br>223.5<br>217.5                                                                                           | 217<br>216.5<br>216.5<br>216.5<br>218.5<br>214.5<br>214.5<br>214.5<br>214.5<br>214.5<br>214.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>213.5<br>21 |
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## ALIGNMENTS

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PPVIAPNAPQPVRIDNPVGGFSFALPAGWVESDAAHFDYGSALLAKTTGDPPFPGQPPPV 120
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Dobos K.M., Khoo K.H., SwiderEK.K.M., Blennan P.J., Belisle J.T.;

Dobos K.M., of the full extent of glycosylation of the 45-kilodalton

"Definition of the Mycobacterium tuberculors.";

J. Bacteriol. 178:2498-2506(1996).

SEQUENCE. 286 AA; 28764 MW; 4BD7ADB9FFB842493 CRC64;
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                                                                                                               Ol-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 25, Last annotation update)
MPT-32=45 kDa CULTURE FILTRATE glycoprotein.
Mycobacterium tuberculosis.
Bacteria, Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
WCBI_TAXID=1773;
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Pred No. 1.3e-89;
1; Mismatches 0;
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Best Local Similarity 99.7
Matches 285; Conservative
                                                                             PRELIMINARY;
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  SASYYEVKFSDPSKPNGQIWTGVIGSPAANAPDAGPPQRWFVVWLGTANNPVDKGAAKAL 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 PPAPATPVAPPPPAA----ANTPNAQ-----PGDPNAAPPP--ADPNAPPPVIAPN 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 PPAAPAPNGQPAPNAQPAPGAPAPNGQPAPAAPAPNDPNAAPPPVGAPPNGAPPPVDPN 114
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                                                                                                                                                                                                                                                              01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Fibronectin-attechment protein FAP-P (Fibronectin-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dheenadhayalan V., Chang Y.F.; "Mycobacterium avium subsp. paratuberculosis fibronectin-binding protein.";
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                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium paratuberculosis.
Bacteria, Actinobacteria, Actinobacteriaco, Corynebacterineae; Mycobacterineae; Mycobacterium.
NCBI_TaxID=1770;
                                               AESIRPLVAPPPPAPAPAPAPAPAPAPAGGVAPTPTTPTPQRTLPA 325
                                                                      241 AESIRPLVAPPPAPAPAPAPAPAPAPAPAGEVAPTTTTPTPQRTLPA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=5781;
SCOOTT T.E., Lin T.L., Wu C.C.;
"Characterization of fibronectin binding by Mycobacterium :
"Characterization";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
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EMBL, AF334165; AAK20394.1; -.
SEQUENCE 368 AA; 36116 MW; 4B22A27730C54337 CRC64;
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                                                                                                                                                                                                                                                                              Mycobacterium paratuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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Schwyzer M., Vloek C., Lowery D.E., Bello L.J., Meyer G.,
Thiry E., Paces V.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194 AA; 19339 MW; 3AEB7CBC893DF292 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schwyzer M., Styger D., Vogt B., Lowery D.E., Simard LaBoissiere S., Misra V., Vlcek C., Paces V.; Vet. Microbiol. 0:0-0(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
NCBL_TaxID=10320;
                                                                       01-WAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Fibronectin-attachment mutant protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32.9%; Score 568; DB 2; 63.9%; Pred. No. 1.3e-28;
194 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 3247 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                281 ESIR---PLVAPPPAP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q65533 PRELIMINARY;
Q6553;
01-NOV-1996 (TEMBLrel. 01,
01-NOV-1996 (TEMBLrel. 01,
01-OCT-2003 (TEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               308 GEVAPTPTTPTPQR 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-179 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bovine herpesvirus 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=COOPER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HERE REPLETED THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF
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Viruses; dsDNA viruses, no RNA st
Alphaherpesvirinae; Simplexvirus.
NCBI_TaxID=10325;
                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 30.7%
nes 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Matches
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Q7T5D9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2755 PTRRAGARKSLPAAQPROKLLRSRSPASVPAPGS----ELVPPPSGGALGSPPSFV---- 2806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2807 -PSRPPSL-----EPVPGLP--LPPSR-----VQAPVDAPAPPPAPERPAPPAP 2848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PATPVAPP-PPAAANTPNAQPGDPNAAPPPADPNAP-----PPPVIAPNAPQPVRID 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LTR----RKGRLAALAIAAMASASLVTVAVPATANADPEPAPPVPTTAASPPSTAAAPPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2644 РАРРЦРРАРРЦРРАРРЦРРАРАГАРУРАРРЦРРРАЦТРАЦТРАРТРАРТРЕВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 NPVGGFSFALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQP-PPVANDTRIVLGRLDQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 LYASAEATDSKAAA----RLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      230 DPSKPNGQIWTGVIGSPAANAPDAGPPQRWFVVWLGTANNPVDKGAAKALABSIRPLVAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                         Schwyzer M., Vlcek C., Lowery D.E., Bello L.J., Meyer G., Misra V.; Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza zativa (Rice).

Gryza zativa (Rice).

Eukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

NCBL_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 12; Length 3247;
                                                                                                 Schwyzer M., Styger D., Vogt B., Lowery D.E., Simard C., LaBoissiere S., Misra V., Vlock C., Paces V.; "Gene contents in a 31-kb segment at the left genome end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 14.8%; Score 256; DB 12; Length 3: Local Similarity 31.2%; Pred. No. 1.4e-07; Local 105; Conservative 20; Mismatches 153; Indels
                                                                                                                                                                                                                                                                                                                                            Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, Z78205; CAB01605.1; -.
EMBL, AJ004801, CAA06097.1 -.
InterPro; IPR06528; Herpes teg N.
InterPro; IPR065210; Herpes Tul36.
Pfam; PF04481; Herpes teg_N, 1.
Pfam; PF0486; Herpes Leg_N, 1.
SEQUENCE 3247 AA, 332190 WW; 3AEAA72P8F001F6A CRC64;
Schwyzer M.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2849 ERPAPPAPERPAPPAPERPAPP----PAPERPAP 2880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            290 P-PAPAPAPAPAPAPAPAGEVAPTPTTPTPQRTLP 324
                                                                                  MEDLINE=97164286; PubMed=9010999;
                                                                                                                                                                       Vet. Microbiol. 53:67-77(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-OCT-2003 (TrEMBLrel. 25,
Hypothetical protein.
                                                 SEQUENCE OF 1-179 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                          STRAIN-JURA;
                                                                                                                                                                                                                                                                                                              STRAIN=JURA;
                                                                                                                                                                                                                                                                                                                                 Schwyzer M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64
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Q9ASK4

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151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       211 SLDANGVSGSASYYEVKFSDPSKPNGQIWTGVIGSPAANAPDAGPPQRWFVVWLGTANNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    171 WAPPMAPSPSGS------PTKP-----SPASPSPIAGDP-----IIPTNNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 AVPATANADPEPAPPVPTTAASPPSTAAAPPAPATPVAPPPAAANTPNAQPGDPNAAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATPATAAAPSTATPTP----ATQPNATPADPSITPPAASPPLPSAATPPPQPDSPPPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92 PADPNAPPPPVIAPNAPQPVRIDNPVGGFSFALPAGWVESDAAHFDYGSALLSKTIGDPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              152 FPGQPPPVANDTRIVLGRLDQKLYASAEATDSKAAARLGSDMGEFYM-PYPGTRINQETV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 SPVQQPPVA-----ASPPPSSPADLPPPNPPAR--SDTPPVVQSPPPHRRSPRTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete Sequence and Comparative Analysis of the Genome of Herpes I Virus (Cercopithecine Herpesvirus 1) from a Rhesus Monkey."; J. Virol. 77:6167-6177(2003). EMBL: AFS33768; AAP41454.1; -SEQUENCE 3288 AA; 342496 MW; 79C391EE8B6F7983 CRC64;
                                                                                                                                                                                                                                          R EMBL; Arvacous,

R Gramene; Q9ASK4; ---

R Gramene; Q9ASK4; ---

R GO; GO:0005524; F:ATP binding; IEA.

R GO; GO:0005474; F:protein serine/threonine kinase activity; IEA.

R GO; GO:0006740; F:protein amino acid phosphorylation; IEA.

R GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

DR INTERPO; IPRO00719; Prot kinase.

DR PRODOM; PRO00001; Prot kinase; 1.

DR PRODOM; PROTEIN KINASE ATP; 1.

DR PROSITE; PS00107; PROTEIN KINASE DOM; 1.

DR PROSITE; PS00101; PROTEIN KINASE DOM; 1.

DR PROSITE; PS00101; ATP-binding; Kinase;

KW Hypothetical protein; ATP-binding; Kinase;

KW Serine/threonine-protein kinase; Transferase.
                                                                                                                     clone:P0439B06.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
EMBL; AP002882; BAB39873.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         271 VDKGAAKALAESIRPLVAPPPAPAPAPAPAPAPAPAPAGEVAPTPTTPQ 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSPLATPSAPGSGTPVVT-PSAPVSGPPSPGTAPATAADRSNKSLSPNTQ 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10; Length 698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=E2490;
MEDLINE=22628476; PubMed=12743273;
Perelygina L., Zhu L., Zurkuhlen H., Mills R., Borodovsky M.,
Hilliard J.K.;
STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Simian herpes B virus (Cercopithecid herpesvirus 1) Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.4%; Score 248.5; DB 10; 30.7%; Pred. No. 7.5e-08; ive 20; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3288 AA.
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01-OCT-2003 (TrEMBLrel. 25, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
Very large tegument protein.
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-----SGDK 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94 -DPNAPPPPVIAPNAPQPVRIDNPVGGFSFALPAGWVESDAAHFDYGSALLSKTTGDPP- 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  210 VSLDANGVSGSASYYEVKFSDPSKPNGQIWTGVIGSPAANAPDAGPPQRWFVVWLGTANN 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------SGDK 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 PATANADPEPAPPVPITAASPPSTAAAPPAPATPVAPPPPAAANTPNAQPGDPNAAPPPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --FPGQPPPVANDTRIVLGRLDQKLYASAEATDSKAAARLGSDMGEFYMPYPGTRINQET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUB=Parotid gland; Kyeyune-Nyombi E., Sands J.F., Oberg K.C., Zhang Q., Szalay A.A., Kyeyune-Nyombi E., Sands J.F., Oberg K.C., Tieche J.-M., Leonora J.; "Cloning and expression of a novel proline-rich protein from porc
                                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               319
                                                                                                                          265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    270 PVDKGAAKALAESIRPLVAPPPAPAPAPAEPAPAPAPAGEVAPTPTTPP 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99; Indels 100;
                                                                       PVDKGAAKALAESIRPLVAPPPAPAPAPAPAPAPAPAPAGEVAPTPTP
                                                                                                                       Bradyrhizobium japonicum.
Bradyrhizobium japonicum.
Bradyrhizobiacese, Bradyrhizobium.
NCBI_TaxID=375;
14.1%; Score 244; DB 6; Length 566; 27.9%; Pred. No. 1.1e-07; ive 10; Mismatches 99; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       parotid glands."; 20 Submitted (MAY-201) to the EMBL/GenBank/DDBJ databases. EMBL; AY035847; AAK61381.1; - GO, GO:0005199; F:structural constituent of cell wall; IEA. InterPro; IPR003882; Pistil extensin. PRI0128; PSTLEXTENSIN. E33B3B5E1BDEB81A CRC64; SEQUENCE 566 AA, $3213 MW; E33B3B5E1BDEB81A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Last annotation update)
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(TrEMBLrel. 24, Last seq
(TrEMBLrel. 25, Last anno
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01-JUN-2003 (TrEM)
01-OCT-2003 (TrEM)
Blr0521 protein.
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                                                                                                                                                                                                                                                                                                                                                                               2972 SLÞTPPSKÞPAFFQPSLATGGSVAPGGDFRRRAPSRPTAAVPAAPSRPPARRLARPAVSR 3031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 PAPPGARPPPGPPP----GPPPPGPAPPGARPPPGPPP---GPPPPGPAPPGARPPPG 124
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                                                                                                                                                                          148 GDPPFPGQP-----PPVANDTRIVLG-----RLDQKLYASAEATDSKAAAR-----LGS
                                                                                                                                                                                                                                                                                                                                                                                                                                  192 DMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFSDPSKPNGQIWTGVIGSPAANAP
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                                                                                                                             30 TVAVPATANADPEPAPPVPTTAASPPSTAAAPPAAATPVAPPPPAAANTPNAQPGDPNAA
                                                                                                                                                                                                                               90 PPPADPNAPPPPV--IAPNAPQPVRIDNPVGGFSFALPAGWVESDAAHFDYGSALLSKTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 PATANADPEPAPPVPTTAASPPSTAAAPPAPATPVAPPPPAAANTPNAQPGDPNAAPPPA
                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Parotid gland, Zhang A., Kyeyune-Nyombi E., Sands J.F., Oberg K.C., Zhang Q., Szalay A.J., Kyeyune-Nyombi E., Sands J.F., Oberg K.C., Tieche J.-M., Leonora J., Conning and expression of a novel proline-rich protein from porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Bukaryota, Metazoga; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Siina; Suidae; Sus.
                                                                             40;
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                             Length 3288;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 parotid glands.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AY035848; ARKG1382.1;
GO; O005199; F:structural constituent of cell wall; IEA.
InterPro; IPR003882; Pist11 extensin.
PRINTS; FR01218; PSTLEXTENSIN.
                                                                       Indels
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Last annotation update)
                          14.4%; Score 248; DB 12; 29.8%; Pred. No. 4.4e-07; ive 24; Mismatches 150;
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Best Local S:
Matches 81
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DB 12; Length 3326;

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Obsawa K., Black D.H., Sato H., Rogers K., Eberle R.,
"Sequence and genetic arrangement of the UL region of the monkey B
virus (Cercopithecine herpesvirus 1) genome and comparison with the
region of other primate herpesviruses.";
Arch. Virol. 148 1989-997 (2003).
EMBL, AB096160; BAC58076.2; -.
SEQUENCE 3326 AA, 345566 MW, 6B53B3860F43CDF0 CRC64;
                                                                                                                             Query Match
Best Local Similarity 29.1%; Pred. No. 1.3e-06;
Matches 93; Conservative 24; Mismatches 162; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             160 ANDTRIVLGRLDQXLYASAEATDSKAA-----ARLGSDMGEFYMPYPG-----TRI 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           206 NQETVSLDANGVSGSASYYEVKFSDPSKPNGQIWTGVIGSPAANAPDAGPPQRWFVVWLG 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47 VPTTAASPPSTAAAPP---APATPVAPPPPAAANTPNAQPGDPNAAPPPADPNAP-PPPV 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ААРООНАРТР----РРРАВРАЯРРАРТРРАРРААВРОНАРРРРАЯВРТРТРРРРРЯ 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 GPAARPT-----PAPTATPTPVAPPPAAPTARPGS-----PAPAATPAPPA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          228 PTATPAPTATPAPGSTP----VRPG 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T---ANNPVDKGAAKALAESIRP--LVAPP----PA--PAPAPAEPAP--APAPAGEVA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPPAAGSPPAPGATPAPTTTPAPGGTATPPSGRPGPASTPAPGAATPAPTATPAPGGALT 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 LAALAIÀAM-----ASASLVTVAVPATANADPEP-----APP----
                             MEDLINE-22484999; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
                                                                                                              "Complete", genomic sequence of nitrogen-fixing symbiotic bacterium tradyrhizobium japonicum USDA110.";

DNA Res. 9:189-197(2020)

EMBL; AP005936; BAC45786.1; -.

EMBL; AP005524; F:ATP binding; IEA.

GO; GO:0004572; F:protein kinase activity; IEA.

GO; GO:0004572; F:protein constituent of cell wall; IEA.

GO; GO:006468; P:protein amino acid phosphorylation; IEA.

InterPro; IPR006665; OmpA/WotB.

InterPro; IPR003882; Pistil extensin.

InterPro; IPR003882; Pistil extensin.

InterPro; IPR003819; Prot_Kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                               115;
                                                                                                                                                                                                                                                                                                                                                                                                DB 16; Length 745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Simian herpes B virus (Cercopithecid herpesvirus 1) (Shbv). Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                                                                                                                                                                                                              14.0%; Score 241.5; DB 16; Length 29.6%; Pred. No. 2.2e-07; ive 16; Mismatches 136; Indels
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MEDLINE=22607624; PubMed=12721804;
                                                                                                                                                                                                                                                                                               Pfam; PP00691; OmpA; 1. PRINTS; PR01218; PSTLEXTENSIN. ProDom; PD000001; Prot_Kinase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                       3055 SRPPARRLARPAVSRSTESFALP-PDELARPRTPEAPAPPTETEEAPVAERPAPPEPPOG 3113
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                                                                                                                                                                                                                                                                                                                                                                                                  133 AAHFDYGSALLSKTTGDPPFPGOP----PPVANDTRIVLG-----RLDQXLYASAEATD 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 SKAAAR-----LGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFSDPSKPNG
                                                                                                                                                                                                                                                                                                                      17 ALAIAAMASASLVTVAVPATANADPEPAPPVPTTAASPPSTAAAPPAPATPVAP--PPPA
    Gaps
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01-MAR.2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
05JNBA0079B05.10 OR OSJNAA0079B05.2.
05TYZA SATIVA (Rice).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyya; Magnoliophyta; Liliopsida; Poales; Poaceae;
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41;
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EMBL; AC079179; AAL31655.1; -.
EMBL; AC116601; AAM08709.1; -.
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Saski C., Henry D., Oates R., Slmmons J.;
"Rice Genomic Sequence.";
submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
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Ming R.A., Yu Y., Yang T.J., Nah G., Soderlund C., C
Rambo T., Saski C., Henry D., Oates R., Simmons J.;
"Rice Genomic Sequence.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                293 PAPAPAEPAPAPAGEVAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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| Db 634PPPPPPPPPBPPPPBPPPPSPPPPPPPPPPPPPPPPP                                                                                  | 677 RIPIGAAISSKGPPPPPPPPLPPANRINGPGVPSAPPPPPPPPANRS       | OY 268 NNPVDKGAAKALAESIRPLVAPPAPAPAPAEPAPAPAPAPAGEVAPTFTTFTPORTL 323 | Db 725 NGPSAPAPPLPPPLPAANKRNPPAPPPPLMTGKKAPAPPPPPPQAPK 773        | Qy 324 P 324                                   | Db 774 P 774                                                           | RESULT 13 Q41805 ID Q41805 PRELIMINARY; PRT; 1188 AA.            | DT 01-NOV-1996 (TrEWBLrel. 01, Created) DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) | Extensin-like protein precursor.<br>Zea mays (Maize).<br>Rikarvota. Viridinlantae. Strentonhyta. | Specmatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. | [1]<br>SEQUENCE FROM N.A.<br>STRAIN=B73; TISSUE=POllen; |                                      | Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.<br>EMBL; 234465; CAA84230.1;<br>PIR; S49915; S49915.                                       | DR Pfam; PF00560; LRR; 3.<br>KW Signal.<br>FT Signal. 1 27 POTENTIAL.<br>SQ SEQUENCE 1188 AA; 120981 MW; 2C77C7F8D7130149 CRC64;                                                                                  | Query Match 13.8%; Score 237.5; DB 10; Length 1188;<br>Best Local Similarity 28.9%; Pred. No. 6.6e-07;<br>Marches 87: Conservative 30: Mismatches 123: Indels 61: Gabs 13; | 34 PATANADEEPAPPVPTTAASPPSTAAAPPAPATPVAPPPAAANTPNAQPGDENAA-                                                                                                           | Qy 92 PADPNA-PPPPVIAPNAPQPVRIDNPVGGFSFALPAGWVESDAAHFDYGSALLSKTTGDP 150 | Db 625 PPAPVASSPPWKSPPPTPVSSPPPPRKSPPPPPAKSTPPPEEYPTPPTSVKSSPP 682                                                                                | Qy 151 PPPGQPPPVANDTRIVLGRLDQKLYASABATDSKAAARLGSDMGBFYMPYPGTRINQETV 210 | 211 SLDANGVSGSASYYEVKFSDPSKPNGOIWTGVIGSPAANAPDAGPPORWFVVWLGTANNP |                                                                             | 271 VDKGAAKALAESIRPLVAPPAPAAPAPAEPAPAPAGEVAPTFTPTPQRIL      | 769 PP | 324 P 32                                                   | AIS & SIS                                  |                                                                         |
|------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------|----------------------------------------------------------------------|-------------------------------------------------------------------|------------------------------------------------|------------------------------------------------------------------------|------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------|---------------------------------------------------------|--------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------|------------------------------------------------------------------|-----------------------------------------------------------------------------|-------------------------------------------------------------|--------|------------------------------------------------------------|--------------------------------------------|-------------------------------------------------------------------------|
| Query Match Best Local Similarity 27.2%; Pred. No. 6.6e-07; Marches 8. Conservative 20.6 Mismarches 121 Thidals 78. Gans 10. | 36 TANADPEPAPPVPTTAASPSTAAAPPAPATPVAPPPAAANTPNAQPGDPNAAPP | 540                                                                  | OY 92PADPNAPPPPVIAPNAPQPVRIDNPVGGFSFALPAGWVESDAAHFDYGSALLSKTT 147 | Db 598 LVPSPPPPPPPPILPNRSVPPPPPPPPPPPPNHSVL633 | Qy 148 GDPPFPGQPPVANDTRIVLGRLDQKLYASAEATDSKAAARLGSDMGEFYMPYPGTRINQ 207 | 208 ETVSLDANGVSGSASYYEVKFSDPSKPNGQIWTGVIGSPAANAPDAGPPQRWFVVWLGTA | 268 NNPVDKGAAKALAESIRPLVAPPPAPAPAPAEPAPAPAPAPAPTTTTTPQRTL                                                                                           | Db 725 NGPSAPAPPLPPPLPAAANKRNFPAPPPPPPPMTGKKAPAPPPPPPQAPK 773                                    | 774 P 77                                                                                                  | RESULT 12<br>07XH56                                     | ID QYXHS6 PRELIMINARY; PRT; 1269 AA. | DT 01-OCT-2003 (TrEMBLrel. 25, Created) DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation undate) | OS Oryza sativa (japonica cultivar-group). OC Eukaryota, Viridiplantea; Streptophyta; Embryophyta; Tracheophyta; OC Supermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; OC Ehrhartoideae; Oryzaee; Oryza. |                                                                                                                                                                            | RA The Rice chromosome 10 Sequencing Consortium; RT "In-depth view of structure, activity, and evolution of rice RT chromosome 10."; R1 Science 300:1566-1569 (2003). |                                                                        | RC SIRAIN=CV. NIPPULLATE; RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.; RT Submitted (Mav2003) to the EMBN/Genbank/DDRI databases |                                                                         | SECUENCE 1209 AM, 1304:51 MM;                                    | Similarity 27.2%; Pred. No. 6.6e-07;<br>2; Conservative 20; Mismatches 121; | 36 TANADPEPAPPVPTTAASPPSTAAAPPAPATPVAPPPBAAANTPNAOPGDPNAAPP |        | 92PADPNAPPPPVIAPNAPQPVRIDNPVGGFSFALPAGWVESDAAHFDYGSALLSKTT | 598 LVPSPPPPPPPPTLPNRSVPPPPPPPPPPPNHSVL598 | OY 148 GDPPFPGQPPPVANDTRIVLGRLDQKLYASAEATDSKAAARLGSDMGEFYMPYPGTRINQ 207 |

RESULT 14

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289 RNSYGDEQVTPAPAAAPAPAPAPAEQAPVAVP-APAPAAPAAPAPDCGSAAPAPAAATD 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169 AAAPAADAPVEQAPVAVPAPAPAAPAPDCGSAAPAAPAPAAPAATDSGYRSKRNSYGDE 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      229 QVTPAPAAAAPAPADAPVEQAPVAVPAPAPVAAPDVECGSAAPAPAAAAAAATDSGYRSK 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           348 SGYRSKRNAYGDEQVTPAPAAABAPADAPV--EQAPVA------VPAPAPTAAPAP 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSKAAARLGSDMG-----EFYMPYPGTR-----INQETVSLDANGVSGSASY 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -GWVESDAAHFDY----GSALLSKTTGDPPFPGQPPPVANDTRIVLGRLDOKLYASAEAT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----PAPDCGS-----AAPAAAPAAAAPA------ATDSGYRSKRNAYG 488
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                                                                                                                                                 Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.4%; Score 231; DB 5; Length 668; 26.4%; Pred. No. 9e-07; tive 23; Mismatches 137; Indels 138;
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                                                                                                                                                                                                                                                                      Waterston R.; "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; science 282:2012-2018(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Waterston R.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AC006672; AAM98004.1;
WormPep, KOBD12.6; CE21047.
Hypothetical protein.
SEQUENCE 668 AA; 62778 MW; FB9ACC5739DC398A CRC64;
                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Bristol N2;
Wu X., Gattung S.;
Whe sequence of C. elegans cosmid KOBD12.";
Submitted (MAR-1999) to the BMBL/GenBank/DDBJ databases.
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                                    01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
KOSD12.6.
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                     668
                   PRT;
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MEDLINE-99069613; PubMed-9851916;
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                PRELIMINARY;
                                                                                                                                   Caenorhabditis elegans
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Best Local Similarity
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Nat. Biotechnol. 21:526-531(2003).

BMB., ABOSO40; BAC75283.1, -

HYPOCHETICAL PROTECTION OF AN SP261 MW; 7AA08D5F87EE2378 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 16; Length 584;
                                                                                              Streptomyces avermitilis.

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

NCBI_TaxID=33903;
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13.4%; Score 230.5; DB 16; Length
Best Local Similarity 29.6%; Pred. No. 8.4e-07;
Matches 94; Conservative 16; Mismatches 113; Indels
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MEDLINE=22608306; PubMed=12692562;
             24, Created)
24, Last sequence update)
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Maximum Match 100%
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US-08-475-414-65
US-08-475-414-65
US-08-65-255-32
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US-09-050-739-70
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## ALIGNMENTS

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CURRATING SYSTEM: PC COMPATIBLE
SOFTWARE: PAPLICATION DATA:
APPLICATION NUMBER: US/08/382,184
FILING DATE: 01-FEB-1995
CLASSIFICATION: 435
ATTORNEY FACENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 22640720
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION 13-2000
                                                                 APPLICANT.
TITLE OF INVENTION: MICROBACTERIAL PROTEINS,
TITLE OF INVENTION: MICROGRANISMS PRODUCING THEM AN
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ADDRESSEE: OBLOW, SPIVAK, MCCLELLAND, MAIER &
ADDRESSEE: OBLOW, SPIVAK, MCCLELLAND, MAIER &
ADDRESSEE: OBLOW, P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Aliginia
COUNTRY: U.S.A.
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100.0%; Pred. No. 6.4e-127;
tive 0; Mismatches 0;
Sequence 2, Application US/08382184; Patent No. 5714593; GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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amino acid
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Best Local Similarity 100.8
Matches 325; Conservative
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APPLICANT: LAQUEYERIE, Anne
APPLICANT: MARCHAL, Gilles
APPLICANT: PESCHER, Pescale
APPLICANT: PESCHER, Pescale
APPLICANT: POMAIN, Felix
TITLE OF INVENTION: MYCOBACTERIAL PROTEINS, MICORORGANISMS PRODUCING THEM
TITLE OF INVENTION: AND THEIR USF FOR VACCINES AND FOR THE DETECTION OF
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 0660-0138-001V
CURRENT APPLICATION NUMBER: US/09/132,528A
CURRENT FILING DATE: 1998-08-11
EARLIER APPLICATION NUMBER: 08/641,356
EARLIER APPLICATION NUMBER: 08/641,356
EARLIER PERCHONS: 5
SOFTWARE: PATCHIN UNCE: 2.1
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100.0%; Pred. No. 6.4e-127;
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; ORGANISM: Mycobacterium tuberculosis
US-09-132-528-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09132528A Patent No. 6221353 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 325; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
US-09-132-528-2
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MICROORGANISMS PRODUCING THEM AND THEIR USE FOR VACCINES
AND FOR THE DETECTION OF TUBERCULOSIS
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                                                                                                                                                                                                                                         GVIGSPAANAPDAGPPQRWFVVWLGTANNPVDKGAAKALAESIRPLVAPPPAPAPAFP 300
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                                                                                                      SFALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPPVANDTRIVLGRLDQKLYASAEA
PPAPATPVAPPPPAAANTPNAQPGDPNAAPPPADPNAPPPVIAPNAPQPVRIDNPVGGF
                         PAPATEVAPPPPAAANTPNAQPGDPNAAPPPADPNAPPPPVIAPNAPPPVIAPNEVGF
                                                                                SPALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPPVANDTRIVLGRLDQKLYASAEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/641,356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 1726; DB 2; Best Local Similarity 100.0%; Pred. No. 6.4e-127; Matches 325; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:

APPLICANT:
TITLE OF INVENTION:
MICROBACTERIAL PROTEINS,
TITLE OF INVENTION: MICROBACTERIAL PROTEINS,
TITLE OF INVENTION: MICROBRANISMS PRODUCING TITLE OF INVENTION: AND FOR THE DETECTION OF TITLE OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEBE: OBLON, SPIVAK, MCCLELLAND, MAIER
ADDRESSEBE: NEUSTADI, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILLNG MALES
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/382,184
FILING DATE: 01-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLOW, NORMAN F
REGISTATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 22640720
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 301 APAPAPAGEVAPTPTTPQRTLPA 325
                                                                                                                                                                                                                                                                                                                            APAPAPAGEVAPTPTTPTPQRTLPA 325
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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10S-08-641-356-2

; Sequence 2, Application US/08641356

; Patent No. 5866130
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amino acid
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MEDIUM TYPE: Floppy
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                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-08-875-494-2
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; EARLIER FILING DATE: 1996-02-01
; EARLIER APPLICATION NUMBER: 382184
; EARLIER FILING DATE: 1995-02-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PATENTIN VET: 2.0
; LENGTH: 325
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Best Local Similarity 100.0%;
Matches 325; Conservative 0
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                                                                                                                                             GENERAL INFORMATION:
APPLICANT: LAQUETRERIE, Anne
APPLICANT: LAQUETRERIE, Anne
APPLICANT: LAQUETRERIE, Anne
APPLICANT: MESCHAL, Gilles
APPLICANT: MESCHAL, Gilles
APPLICANT: MESCHAL, MECASA
TITLE OF INVENTION: MYCOBACTERIAL PROTEINS, MICORORGANISMS PRODUCING THEM
TITLE OF INVENTION: TUBERCULOSIS
TITLE OF INVENTION: TUBERCULOSIS
TITLE OF INVENTION: TUBERCULOSIS
TITLE OF INVENTION: TUBERCULOSIS
TITLE OF INVENTION: TUBERCULOSIS
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TITLE OF INVENTION: TUBERCULOSIS
TITLE OF INVENTION: TUBERCULOSIS
TITLE OF INVENTION: 1998-00-11
EARLIER APPLICATION NUMBER: 08/641,356
SARIER PILING DATE: 1996-04-30
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATENTIN VOFT. 2.1
SEQ ID NO 3
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APPLICANT: MARCHATION:
APPLICANT: MARCHAL, GILLES
APPLICANT: PESCHER, PASCALE
APPLICANT: PESCHER, PASCALE
APPLICANT: ROMAIN, FELIX
TITLE OF INVENTION: MYCOBACTERIAL PROTEINS, MICROORGANISMS PRODUCING THEM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 0660-0122-0 PCT
CURRENT APPLICATION NUMBER: US/08/975,494
CURRENT FILLING DATE: 1997-08-01
EARLIER APPLICATION NUMBER: PCT/FR96/00166
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100.0%; Pred. No. 6.4e-127;
ive 0; Mismatches 0;
301 APAPAPAGEVAPTPTTPTPQRTLPA 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT , ORGANISM: Mycobacterium tuberculosis US-09-132-528-3
                                                                                                          Sequence 3, Application US/09132528A
Patent No. 6221353
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Matches 325; Conservative
                                                                                       US-09-132-528-3
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Sequence 2, Application US/0959366

Facent No. 6335181

GENERAL INFORMATION:

APPLICANT: LAGUERRELE Anne

APPLICANT: MARCHAL, Gilles

APPLICANT: RCMAIN, Felix

APPLICANT: RCMAIN, Felix

TITLE OF INVENTION: MYCOBACTERIAL PROTEINS, MICORORGANISMS PRODUCING THEM

TITLE OF INVENTION: MYCOBACTERIAL PROTEINS, MICORORGANISMS PRODUCING THEM

TITLE OF INVENTION: MYDERCULOSIS

TITLE OF INVENTION: TUBERCULOSIS

TITLE OF INVENTION: TUBERCULOSIS

TITLE OF INVENTION: TUBERCULOSIS

TITLE OF INVENTION: 105/09/599,366

CURRENT APPLICATION NUMBER: 09/132,228

FRIOR APPLICATION NUMBER: 09/132,228

FRIOR PAPLICATION NUMBER: 09/413,356

FRIOR PILING DATE: 1996-04-30

NUMBER OF SEQ ID NOS: 5

SOFTWARE: Patentin Ver: 2.1

SEQ ID NO 2

LENGTH: 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 GVIGSPAANAPDAGFPQRWFVVWLGTANNPVDKGAAKALAESIRPLVAPPRAPAPAFPF 300
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                                                                Gaps
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      Length 325;
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                                                             Indels
Score 1726; DB 3;
Pred. No. 6.4e-127;
Mismatches 0;
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Sequence 2, Application US/08875494
; Sequence 2, Application US/08875494
; Sequence 2, Application US/08875494
; Patent No. 6379902
; GENERAL INFORMATION:
; APPLICANT: HAGUETERIE, ANNE
; APPLICANT: PESCHER, PASCALE
; APPLICANT: POWAIN, FELIX
; TITLE OF INVENTION: MYCOBACTERIAL PROTEINS, MICROORGANISMS PRODUCING THEM
; TITLE OF INVENTION: TUBERCULOSIS
; TITLE OF INVENTION: TUBERCULOSIS
; TITLE OF INVENTION: TUBERCULOSIS
; TITLE OF INVENTION: TUBERCULOSIS
; TITLE OF INVENTION NUMBER: US/08/875,494
; CURRENT APPLICATION NUMBER: DS/08-01
; PRIOR APPLICATION NUMBER: PCT/FR96/00166
; PRIOR APPLICATION NUMBER: 382184
; PRIOR FILING DATE: 1996-02-01
; PRIOR APPLICATION NUMBER: 382184
; SOFTWARE: PATENT Ver. 2.0
; SEQ ID NOS: 4
; SOFTWARE: PATENTIN Ver. 2.0
; TANGTH. 30-01
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Patent No. 6638518
GENERAL INFORMATION:
GENERAL INTORMATION:
APPLICANT: Rathiff, Timothy
APPLICANT: Kline, Joel
TITLE OF INVENTION: METHOD FOR INHIBITING INFLAMMATORY RESPONSES
FILE REPERRING: 140.0010 0101
CURRENT APPLICATION UNDER: US/09/510,031A
CURRENT FILING DATE: 2000-02-22
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Local Similarity 100.0%; Pred. No. 6.4e-127;
tes 325; Conservative 0; Mismatches 0;
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                                           301 APAPAPAGEVAPTPTTPTPQRTLPA 325
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TYPE: PRI
ORGANISM: Mycobacterium tuberculosis
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APPLICANT: LAQUERERIE, Anne
APPLICANT: MARCHAL, Gilles
APPLICANT: PESCHER, Pascale
APPLICANT: PESCHER, Pascale
APPLICANT: PESCHER, Pascale
APPLICANT: PESCHER, PELICAN
TITLE OF INVENTION: MYCOBACTERIAL PROTEINS, MICORORGANISMS PRODUCING THEM
TITLE OF INVENTION: AND THEIR USE FOR VACCINES AND FOR THE DETECTION OF
TITLE OF INVENTION: TUBERCULOSIS
TITLE OF INVENTION: TUBERCULOSIS
TITLE OF INVENTION: UMBER: US/09/599,366
CURRENT APPLICATION NUMBER: US/09/599,366
CURRENT APPLICATION NUMBER: 00/132,528
PRIOR FILING DATE: 1998-08-11
PRIOR PELING DATE: 1998-08-11
PRIOR PELING DATE: 1998-04-30
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
TUBER OF SEQ ID NO 3
TUBER OF SEQ ID NO 3
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100.0%; Score 1726; DB 4;
Best Local Similarity 100.0%; Pred. No. 6.4e-127;
Matches 325; Conservative 0; Mismatches 0;
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Patent No. 6335181
GENERAL INFORMATION:
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LENGTH: 325
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| Sequence 2, Application US/09985372
| Patent No. 6676945
| Patent No. 6676945
| GENERAL INPORMATION:
| APPLICANT: LAQUETRERIE, Anne
| APPLICANT: PESCHER, Pascale
| APPLICANT: PESCHER, Pascale
| APPLICANT: PESCHER, Pascale
| APPLICANT: POWAIN, Pelix
| TITLE OF INVENTION: AND THERE USE FOR VACCINES AND FOR THE DETECTION OF
| TITLE OF INVENTION: TUBERCULOSIS
| FILE REFERENCE: 0660-0138-0DIV
| CURRENT APPLICATION NUMBER: US/09/985,372
| CURRENT APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 09/132,528
| PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-11
| NUMBER OF SEQ ID NOS: 5
| SOFTWARE: PATENTIN VET. 2.1
| SEQ ID NO 2
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                                                                                                                                                                     Length 325;
                                                                                                                                                                                                     Indels
                                                                                                                                                                  100.0%; Score 1726; DB 4;
100.0%; Pred. No. 6.4e-127;
ive 0; Mismatches 0;
PRIOR APPLICATION NUMBER: US 60/121,177
PRIOR FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
LENGTH: 325
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
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Best Local Similarity 100.
Matches 325; Conservative
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Matches 325; Conservative
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US-09-510-031A-6
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Sequence 3. Application US/09985372
| Sequence 3. Application US/09985372
| Patent No. 6676945
| GENERAL INFORMATION:
| APPLICANT: BASCHER, Pascale
| APPLICANT: BASCHER, Pascale
| APPLICANT: ROMAIN: Felix
| TITLE OF INVENTION: MYCOBACTERIAL PROTEINS, MICORORGANISMS PRODUCING THEM
| TITLE OF INVENTION: MYCOBACTERIAL PROTEINS, MICORORGANISMS PRODUCING THEM
| TITLE OF INVENTION: WYCOBACTERIAL PROTEINS, MICORORGANISMS PRODUCING THEM
| TITLE OF INVENTION: WOMBER: US/09/986,372
| FILE REFERENCE: 066-0138-0DIV
| CURRENT APPLICATION UNMERR: US/09/986,372
| PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/132,528
| PRIOR PILING DATE: ERRLIER FILING DATE: 1998-08-11
| NUMBER OF SEQ ID NOS: 5
| SOFTWARE: PATENTIN Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 325; Conserv
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APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Wedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Carpotal Compounds APPLICANT: Wedvick, Daniel R.
APPLICANT: Wedvick, Daniel R.
APPLICANT: Wardzik, Daniel R.
APPLICANT: Wardzik, Daniel R.
CORRESPONDENCES: 148
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFUTER: TENDED disk
COMPUTER: IBM PC compatible
CONFORTER: PACHOLIS FOR COMPANION
SYSTEM: PC-DOS/MS-DOS
SOFTWARE PACHOLIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
FILING DATE: 1-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MAKi, David J.
REGISTRATION NUMBER: 210121.417C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 53:
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100.0%; Score 1726; DB 4;
Best Local Similarity 100.0%; Pred. No. 6.5e-127;
Matches 325; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                               6300 Columbia Center, 701 Fifth Avenue
308 APAPAPAGEVAPTPTTPTPQRTLPA 332
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                                                                                                               Sequence 53, Application US/08818111
Patent No. 6338852
                                                                                                                                                                                                                                                                                                                                                                                                                         SEED and BERRY LLP
                                                                                                                                                                                APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 332 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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SEQUENCE CHARACTERISTICS:
LENGTH: 332 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Seattle
STATE: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
CITY: Se
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                                                         Sequence 53, Application US/08818112
Patent No. 6290969
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Olllon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF TUBERCULOSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IEM PC Compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
A.PLICATION NUMBER: US/08/818,112
FILING DATE: 13 *MAR-1997
CLESSIFICATION: 42-1997
                                                                                                                                                                                                                                                                                                                                                                                                  E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APAPAPAGEVAPTPTTPTPQRTLPA 325
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
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TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 53: SEQUENCE CHARACTERISTICS: LENGTH: 332 amino acids
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Matches 325, Conservative
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ADDRESSEE: SEED and I
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                                                                                                                      GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Bacid, Steven G.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, Daniel R.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Hendrickson, Ronald C.
ITILE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
ITILE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DoS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FLING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAK!, David J. 392
REJERRACE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 53:
SEQUENCE CREARACTERISTICS:
LENGTH: 332 amino acids
TWOSE AMINORALICS:
LENGTH: 332 amino acids
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                                                                          ; Sequence 53, Application US/09072596
; Patent No. 6458366
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STRANDEDNESS: si:
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CITY: Seattle
STATE: Washingt
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                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A W.
APPLICANT: Steiky, Yasir A W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 1726; DB 4; Length 332; 100.0%; Pred. No. 6.5e-127; ive 0; Mismatches 0; Indels 0
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COUNTRY: USA

ZIP: 98144-7092

ZIP: 98144-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION: NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
FELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-693
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
FENCHT: 332 amino acids
APAPAPAGEVAPTPTTPQRTLPA 325
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US-09-056-556-53
Sequence 53, Application US/09056556
Patent No. 6350456
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Matches 325; Conservative
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STATE: Washington
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Thu Jul 8 11:11:31 2004

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Search completed: July 7, 2004, 18:24:53 Job time: 17.5 secs

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July 7, 2004, 18:24:06; Search time 42.5 Seconds (without alignments) 2380.406 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                       US-10-720-192-3
                                                                                                                                                                                                                                                                                                                                                                           Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
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                                                                                                                                                                                                         Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Description                   | Sequence 2, Appli<br>Sequence 3, Appli<br>Sequence 53, Appli<br>Sequence 53, Appl<br>Sequence 63, Appl<br>Sequence 11, Appl<br>Sequence 350, Appl<br>Sequence 350, Appl<br>Sequence 20, Appl<br>Sequence 20, Appl<br>Sequence 20, Appl<br>Sequence 214, Appl<br>Sequence 346, Appl<br>Sequence 346, Appl<br>Sequence 314, Appl |
|-------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| SUMMARIES                     | US-09-985-372-2<br>US-09-985-372-3<br>US-09-985-372-3<br>US-10-193-002-53<br>US-10-098-732A-41<br>US-10-193-702-4<br>US-10-193-702-4<br>US-10-193-702-209<br>US-10-193-002-209<br>US-10-193-002-209<br>US-10-193-002-209<br>US-10-193-002-209<br>US-10-193-002-346<br>US-10-184-843-2514<br>US-10-084-843-2514<br>US-10-084-843-2514<br>US-10-1359-460-10                                                                                                          |
| DB                            | ;<br>; qqqqqqqqqqqqqq<br>; qqqqqqqqqqqqqqqqqq                                                                                                                                                                                                                                                                                                                                                                                                                      |
| %<br>Query<br>Match Length DB |                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| %<br>Query<br>Match           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| Score                         | 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1                                                                                                                                                                                                                                                                                                                                                                                                                              |
| Result<br>No.                 | 1 1 2 6 4 7 7 7 8 9 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1                                                                                                                                                                                                                                                                                                                                                                                                          |

| 841001411<br>849061111                                                                                                                                       | ence 14222<br>ence 12405<br>ence 124927<br>ence 12810<br>ence 16286<br>ence 3364,<br>ence 18454 | equence 161137,<br>equence 167716,<br>equence 123256,<br>equence 19519,<br>equence 19554,<br>equence 19554,<br>equence 18982,<br>equence 18982,<br>equence 18983,<br>equence 18983,<br>equence 1813, Ap |
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| 10-437-963-18476<br>10-437-963-14131<br>10-437-963-16876<br>10-437-963-16998<br>10-425-114-41545<br>10-437-963-10257<br>10-437-963-10257<br>10-437-963-10257 | -963-14<br>-761-12<br>-963-14<br>-963-12<br>-963-16<br>-122A-6<br>-963-12                       | 10-437-963-16113<br>10-437-963-16113<br>10-437-963-12225<br>10-437-963-12225<br>10-437-963-19511<br>10-437-963-19511<br>10-437-963-1959<br>10-437-963-1599<br>10-437-963-1599<br>10-437-963-12598       |
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| 248.5<br>240.5<br>240.5<br>240.5<br>233.5<br>233.5<br>233.5                                                                                                  | 200.<br>200.<br>200.<br>200.<br>200.                                                            | 223.75<br>223.75<br>221.5<br>220.5<br>220.5<br>219.5<br>218.5<br>218.5<br>217.5                                                                                                                         |
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## ALIGNMENTS

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Sequence 2, Application US/0998372

Publication No. US20030054008A1

GENERAL INFORMATION:

APPLICANT: LAQUENTERIE, Anne
APPLICANT: LAQUENTERIE, Anne
APPLICANT: PESCHER, Pascale
APPLICANT: PESCHER, Pascale
APPLICANT: ROMAIN, Felix
ITLE OF INVENTION: MYCOBACTERIAL PROTEINS, MICORORGANISMS PRODUCING THEM
ITLE OF INVENTION: WYCOBACTERIAL PROTEINS, MICORORGANISMS PRODUCING THEM
ITLE OF INVENTION: WYCOBACTERIAL PROTEINS, AND FOR THE DETECTION OF
ITLE OF INVENTION: UNMERR: US/09/985,372

CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1998-08-11

NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATENTIN OF: 2.1

SEQ ID NO 2
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100.0%; Score 1726; DB 10; Length 325;
Best Local Similarity 100.0%; Pred. No. 8.6e-106;
Matches 325; Conservative 0; Mismatches 0; Indels 0;
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-09-985-372-2
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181 IDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEVKFSDPSKPNGQIWT 240
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GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir
APPLICANT: Reed, Steven
APPLICANT: Reed, Steven
APPLICANT: Reed, Steven
APPLICANT: Reed, Steven
APPLICANT: Reed, Steven
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
FILE REFERENCE: 014058-0097005
FILE REFERENCE: 014058-0097005
FILE REFERENCE: 2001-06-20
FRICK APPLICATION NUMBER: US 09/597,796
FRICK APPLICATION NUMBER: US 09/597,796
FRICK APPLICATION NUMBER: US 00/265,737
FRICK FILING DATE: 2001-02-01
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentIn Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 1726; DB 12; Length 332; 100.0%; Pred. No. 8.7e-106; Live 0; Mismatches 0; Indels 0;
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ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Skeiky, Yasir A.W.
Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonia
Houghton, Paymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND ME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
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Best Local Similarity 100.
Matches 325; Conservative
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US-09-886-349A-41
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                     SFALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPPVANDTRIVLGRLDQKLYASAEA 180
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APPLICANT: MARCHAL, Gilles
APPLICANT: RESCHER, Pascale
APPLICANT: RESCHER, Pascale
APPLICANT: RESCHER, Pascale
APPLICANT: RESCHER, Pascale
APPLICANT: ROMAIN, Felix
TITLE OF INVENTION: MYCOBACTERIAL PROTEINS, MICORORGANISMS PRODUCING THEM
TITLE OF INVENTION: TUBERCULOSIS
FILLE REPERENCE: 0660-0138-010V
CURRENT APPLICATION NUMBER: US/09/985,372
CURRENT APPLICATION NUMBER: US/09/985,372
PRIOR RILING DATE: 2001-11-02
PRIOR PILING DATE: 2001-11-02
PRIOR FILING DATE: EALLER APPLICATION NUMBER: 09/132,528
PRIOR FILING DATE: EALLER FILING DATE: 1998-08-11
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; LENGTH: 325
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-985-372-3
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US-09-886-349A-41
, Sequence 41, Application US/09886349A
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Best Local Similarity 100.0
Matches 325; Conservative
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Lodes, Michael J.
Hendrickson, Ronald C.
INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 53: US-10-084-843-53
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; Sequence 41, Application US/10098732A
; Publication No. US20030175294A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 332 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 53:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                      CITY: Seattle
STATE: Washington
COUNTRY: USA
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Best Local Similarity 100.0
Matches 325; Conservative
                                                                             NUMBER OF SEQUENCES:
                                       TITLE OF
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                                                                                                          COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-Jul-2002
CLASSIFICATION > CURROWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
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100.0%; Pred. No. 8.7e-106;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                               NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 53:
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Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
                                 COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 53, Application US/10084843
Publication No. US20030143243A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Skeiky, Yasir A.W.
Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 332 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 325; Conserva
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US-10-084-843-53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 332;
                                                                                                                                                   COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COPEATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/10/084,843

FILING DATE: 25-Feb-2002

CLASSIFCATION NUMBER: US/09/072,967

FILING DATE: 05-MAY-1998

ATTORNEY/AGENT INPORMATION:

NINMEN APPLICATION NUMBER: US/09/072,967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ĎB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 1726; DB 14;
100.0%; Pred. No. 8.7e-106;
live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
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Publication No. US20030054008A1

SEQUENCE A. INFORMATION:

APPLICANT: LAQUEYERER: Anne

APPLICANT: PESCHER, Pascale

APPLICANT: RESCHER, Pascale

APPLICANT: ROMAIN, Felix

TITLE OF INVENTION: MYCOBACTERIAL PROTEINS, MICORORGANISMS PRODUCING THEM

TITLE OF INVENTION: TUBERCULOSIS

FILE REFERENCE: 0660-0138-0DIV

CURRENT APPLICATION NUMBER: US/09/985,372

CURRENT APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/132,528

PRIOR APPLICATION DATE: EARLIER FILING DATE: 1998-08-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120
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APPLICANT: Skeiky, Yasir
APPLICANT: Brannon, Mark
APPLICANT: Guderian, Jeffrey
APPLICANT: Guderian, Jeffrey
TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
TITLE OF INVENTION: Heterologous Fusion Protein Constructs
TITLE OF INVENTION: Leishmania Antigen
FILE REFERENCE: 014058-01201008;
CURRENT APPLICATION NUMBER: US/10/098,732A
CURRENT APLICATION NUMBER: US 60/275,837
PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 80
SEQ ID NOS: 80
LENGTH: 332
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                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Description of Artificial Sequence:DPEP
US-10-098-732A-41
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                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 286
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US-09-985-372-4
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                                                                                                                                                                                                                                                                                                       61 PPVIAPNAPQPVRIDNPVGGFSFALPAGWVESDAAHFDYGSALLSKTIGDPPFPGQPPPV
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                                                                                                                                                                40 DPEPAPPVPTTAASPPSTAAAPPAPATPVAPPPPAAANTPNAQPGDFNAAPPPADFNAPP
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                                                                                                                     Gaps
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                                                                    Length 286;
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Dillon, Davin C.
Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 AESIRPLVAPPPAPAPAPAEPAPAPAPAGEVAPTPTTPTPQRTLPA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 AESIRPLVAPPPAPAPAPAPAPAPAPAPAGEVAPTPTTPTPQRTLPA 325
                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Version #1.30
                                                               Query Match 89.3%; Score 1542; DB 10;
Best Local Similarity 100.0%; Pred. No. 9.3e-94;
Matches 286; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-Jul-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 350, Application US/10193002
Publication No. US20030135026A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 350
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 350
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US-10-193-002-350
       ; ORGANISM: My
US-09-985-372-4
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Query Match
Best Local Similarity 100.
Matches 279; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION: APPLICANT: Reed, S
                                                                                                                                                                                                                         US-10-084-843-355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KFSDPSKPNGQIWTGVIGSPAANAPDAGPPQRWFVVWLGTANNPVDKGAAKALAESIRPL 286
                                                                                                                                                                                                                                                                                                                         107 APQPVRIDNPVGGFSFALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPPVANDTRIV 166
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                                                                                                                                                                                                       Gaps
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Lodes, Michael J.
Hendrickson, Ronald C.
INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
INVENTION: COMPOUNDS OF TUBERCULOSIS
                                                                                                                                                                                                     0
                                                                                                                                                                 Length 652;
                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          614 VAPPPAPAPAPAPAPAPAGEVAPTPTTPORTLPA 652
                                                                                                                                                            86.8%; Score 1499; DB 14;
100.0%; Pred. No. 1.5e-90;
ive 0; Mismatches 0;
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REFERENCE/DOCKET NUMBER: 210121.411C9
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ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Ver

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 18/10/084,843

FILING DATE: 25-Feb-2002

CLASSIFICATION: <Unknown>
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APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INPORMATION:
                                                                    ) MOLECULE TYPE: DIOLEM
) SEQUENCE DESCRIPTION: SEQ ID NO: 350:
US-10-193-002-350
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ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center,
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Dillon, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
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Sequence 355, Application US/10084843

Publication No. US20030143243A1

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.
LENGTH: 652 amino acids
                   TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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STATE: Washington
                                                                                                                                                                                al Similarity 100.
279; Conservative
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                                                                                                                                                            Query Match
Best Local S:
Matches 279
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APPLICANT: SHENKY, MASHIY A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Alderson, Mark
APPLICANT: Alderson, Mark
APPLICANT: Corixa Corporation
TITLE OF INVENTION: and Their Uses
TITLE OF INVENTION: and Their Uses
TITLE OF INVENTION: and Their Uses
TITLE OF INVENTION: DATE: 1990-02.03
CURRENT APPLICATION NUMBER: US/09/287,849
CURRENT APPLICATION NUMBER: US 08/818,112
PRIOR APPLICATION NUMBER: US 08/942,578
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,556
PRIOR APPLICATION NUMBER: US 09/025,566
PRIOR APPLICATION NUMBER: US 09/025,23,040
PRIOR APPLICATION NUMBER: US 09/223,040
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100.0%; Pred. No. 1.5e-90;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 355:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-287-849-10
; Sequence 10, Application US/09287849
; Patent No. US20020009459A1
TELEPHONE: (206) 622-491
TELEFAX: (206) 682-6031
INFORMATION FOR SEC ID NO: 355:
SEQUENCE CHARACTERISTICS:
                                                                                                                                              LENGTH: 652 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Skeiky, Yasir A.W.
Dillon, Davin C.
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Gaps

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107 APQPVRIDNPVGGFSFALPAGWVESDAAHFDYGSALLSKTTGDPPFGQPPPVANDTRIV 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  524 VPTTAASPPSTAAAPPAPPATPVAPPPPAAANTPNAQPGDPNAAPPPADPNAPPPVIAPN
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                                                                                                                                                      Length 802;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/193,002
FILING DATE: IO-Jul-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
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                                                                                                                                                  86.8%; Score 1499; DB 14;
100.0%; Pred. No. 1.9e-90;
ive 0; Mismatches 0;
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REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
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FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
                          TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 209:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Skalky, Yasir A.W.
Skalky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonia
Houghton, Raymond
Vadvick, Thomas S.
Twadzik, Daniel R.
Lodes, Michael J.
Lodes, Michael J.
Hendrickson, Romald C.
TITLE OF INVENTION: COMPOUNDS AND ME.
TUBERCULOSIS
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Publication No. US20030135026A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
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ZIF: 98104-7092.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STRANDEDNESS: single
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                                                                                                                                                                                      Best Local Similarity 100.
Matches 279; Conservative
                                                                                                                                                                                   Similarity
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US-10-193-002-209
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                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47 VPTTAASPPSTAAAPPAPATPVAPPPAAANTPNAQPGDPNAAPPPADFNAPPPPVIAPN 106
                                                                                                                                                                                                                                                                              107 APQPVRIDNPVGGFSFALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPPVANDTRIV 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                              644 LGRLDOKLYASABATDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEV 703
                                                                                                                                                                                                          524 VPTTAASPPSTAAAPPAPAPAPPPAAANTPNAQPGDPNAAPPPADPNAPPPVIAPN
                                                                                                                                                                                                                                                                                                                                                                                                          LGRLDQKLYASAEATDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEV
                                                                                              Gaps
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Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Rorald C.
Hendrickson, Romald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                          Length 802;
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STREET: 6300 Columbia Center, 701 Fifth Avenue STREET: 6300 Columbia Center, 701 Fifth Avenue STRIET: 84104 Fifth Avenue STRIE: 98104-7092
COUNTRY: USA
ZIP: 98104-7092
COMPUTER: 18 PR PC compatible COMPUTER: 18 PR PC compatible COMPUTER: 18 PR PC compatible COMPUTER: 18 PR PC COMPUTER: 18 PC COMPUTER: 18 PR PC COMPUTER: 18 PC COMPUTER: 18 PC COMPUTER: 18 PC COMPUTER: 18 PC COMPUTER: 18 PC COMPUTER: 18 PC COMPUTER: 18 PC COMPUTER: 18 PC COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUTER: 10 COMPUT
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                          86.8%; Score 1499; DB 9;
100.0%; Pred. No. 1.9e-90;
:ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 210121.417C9 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Maki, David J. REGISTRATION NUMBER: 31,392
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Dillon, Davin C.
Campos-Neto, Antonia
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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 209:
SEQUENCE CHARACTERISTICS:
LENGTH: 802 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 209, Application US/10193002
Publication No. USZ0030135026A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
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                                Query Match 86.8
Best Local Similarity 100.
Matches 279; Conservative
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US-10-193-002-209
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47 VPTTAASPPSTAAAPPAPATPVAPPPPAAANTPNAQPGDPNAAPPPADPNAPPPVIAPN 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               524 VPITAASPPSTAAAPPPAPATPVAPPPPAAANTPNAQPGDPNAAPPPPADPNAPPPPVIAPN
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Skalky, Yasir A.W.
Skalky, Yasir A.W.
Dillon, Davin C.
Campos Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPATER: IBM PC Compatible
COMPATES: PATENT: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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ilarity 100.0%; Pred. No. 1.9e-90;
Conservative 0; Mismatches 0;
                                       REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEFAX: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Peb-2002
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 214:
08-10-084-843-214
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CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
REGISTRATION NUMBER: 31,392
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Publication No. US20030143243A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                             LENGTH: 802 amino acids
TYPE: amino acid
STRANDEDNESS: single
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STATE: Washington
COUNTRY: USA
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Best Local Similarity
Matches 279; Conserv
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US-10-084-843-351
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Lodes, Michael J.
Hendrickson, Romald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: DAYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US/10/084,843

FILING DATE: 25-Feb-2002

CLASSIFICATION: <unimal control of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the co
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                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 802 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: procesin
SEQUENCE DESCRIPTION: SEQ ID NO: 346:
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ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center,
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Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
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    INFORMATION FOR SEQ ID NO: 346:
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STATE: Washington
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US-10-084-843-214
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SEQ ID NO 10
LENGTH: 802
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Publication No. US2000147911A1

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Blilon, Davin C.

APPLICANT: Campos-Meto, Antonio

CURRENT: Compos-Meto, Antonio

CURRENT APPLICATION NUMBER: US/08/287,849

PRIOR FILING DATE: 1999-04-07

PRIOR PRIOR APPLICATION NUMBER: US 08/942,578

PRIOR PRIOR APPLICATION NUMBER: US 08/942,578

PRIOR PRIING DATE: 1998-04-07

PRIOR PRIING DATE: 1998-04-07

PRIOR PRIING DATE: 1998-04-07

PRIOR PRIING DATE: 1998-04-07

PRIOR FILING DATE: 1998-04-07

PRIOR FILING DATE: 1998-04-07

PRIOR FILING DATE: 1998-12-30

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                                                                                                                    REFERENCE/DOCKET NUMBER: 210121.411C9 TELECOMMUNICATION INFORMATION:
APPLICATION NUMBER: US/09/072,967
                                                                                                                                                                                                                                                                                                 TRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 351:
US-10-084-843-351
                                                                                           REGISTRATION NUMBER: 31,392
                                                                                                                                                               TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 351:
SEQUENCE CHARACTERISTICS:
LENGTH: 802 amino acids
                      FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
                                                                                                                                                                                                                                                                                         TYPE: amino acid
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US-10-359-460-10
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                                                                                                                                                                                                                                                                                                                                                                                                           524 VPITAASPPSTAAAPPAPATPVAPPPPAAANTPNAQPGDPNAAPPPADPNAPPPVIAPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  644 LGRLDQKLYASAEATDSKAAARLGSDMGEFYMPYPGTRINQETVSLDANGVSGSASYYEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 APQPVRIDNPVGGFSFALPAGWVESDAAHFDYGSALLSKTTGDPPFPGQPPPVANDTRIV
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                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence:tetra-fusion US-10-359-460-10
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0
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86.8%; Score 1499; DB 14;
Best Local Similarity 100.0%; Pred. No. 1.9e-90;
Matches 279; Conservative 0; Mismatches 0;
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Job time : 61.5 secs
                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
SOFTWARE: Patentin Ver. 2.1
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